WEST Search History

DATE: Monday, January 23, 2006

Hide?	Set Name	Query	Hit Count
		DB=PGPB,USPT,EPAB; PLUR=YES; OP=OR	
☐	L34	L27 and probe	1
☐	L33	L27 and complementary	0
☐	L32	6316272.pn.	1
☐	L31	L30 not @ay>2001	20
☐	L30	L1 and (prostate or colon)	39
☐	L29	L28 not @ay>2001	20
☐	L28	L3 and (prostate or colon)	39
☐	L27	6794501.pn.	1
☐	L26	6794501.pn	0
☐	L25	L24 and L1	0
☐	L24	colorectal.ti.	208
☐	L23	L22 and (prostate or colon)	0
☐	L22	6235879.pn.	1
☐	L21	L20 and L14	2
☐	L20	L19 and L12	4
☐	L19	(ross or mizukami or Rao).in.	21320
☐	L18	L2 and L12	6
☐	L17	L13 and (prostate or colon)	3
☐	L16	L15 and (prostate or colon)	2
☐	L15	L13 and L14	2
☐	L14	L2.clm.	37914
☐	L13	L3 and L12	6
☐	L12	L7 or L8 or L10	8
☐	L11	L7 or L8 or L10L10	5
☐	L10	L1.ab.	7
☐	L9	L1.ab. L8	8
☐	L8	L1.ti.	4
☐	L7	L1.clm.	3
☐	L6	L5 and (screen$ or detect$ or determin$ or diagnos$)	34
☐	L5	L3 and L4	34
☐	L4	@AY <= 2001	5488050

☐	L3	L1 and L2	70
☐	L2	cancer$ or neoplas$ or angiogen$ or tumor$	184538
☐	L1	hip1 or (huntington adj interacting adj protein)	81

END OF SEARCH HISTORY

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                        GenCore version 5.1.6
                Copyright (c) 1993 - 2006  Compugen Ltd.


OM nucleic - nucleic search, using sw model

Run on:             January 10, 2006, 11:00:20 ; Search time 14682 Seconds
                                              (without alignments)
                                              17554.026 Million cell updates/sec

Title:              US-10-007-047-1
Perfect score:      4534
Sequence:           1 ccaagcttggtacccccggg..........gcatgcnntagagggccccta 4534

Scoring table:      OLIGO_NUC
                    Gapop 60.0 , Gapext 60.0

Searched:           5883141 seqs, 28421725653 residues

Word size :         0

Total number of hits satisfying chosen parameters:      11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :          GenEmbl:*
                    1:  gb_ba:*
                    2:  gb_in:*
                    3:  gb_env:*
                    4:  gb_om:*
                    5:  gb_ov:*
                    6:  gb_pat:*
                    7:  gb_ph:*
                    8:  gb_pr:*
                    9:  gb_ro:*
                    10:  gb_sts:*
                    11:  gb_sy:*
                    12:  gb_un:*
                    13:  gb_vi:*
                    14:  gb_htg:*
                    15:  gb_pl:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES
                     %
Result            Query
  No.    Score  Match Length DB  ID                          Description
  ---------------------------------------------------------------------------
       1   3035   66.9   4714  8  HSU79734                    U79734 Human hunti
       2   3035   66.9   6626  6  AX828392                    AX828392 Sequence
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	3	3028	66.8	4707	6	CQ728008	CQ728008 Sequence
	4	2940	64.8	3093	8	AF365404	AF365404 Homo sapi
	5	2619	57.8	4796	6	AR153626	AR153626 Sequence
	6	2619	57.8	4796	6	BD227037	BD227037 Apoptosis
	7	1162	25.6	1201	8	HSHIPIPRO	Y09420 H.sapiens m
	8	973	21.5	134979	8	AC018720	AC018720 Homo sapi
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	10	955	21.1	3715	6	BD227072	BD227072 Apoptosis
	11	955	21.1	3715	8	HSAHIPI28	AF052288 Homo sapi
c	12	922	20.3	180399	14	AC079252	AC079252 Homo sapi
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	14	907	20.0	1164	6	BD227036	BD227036 Apoptosis
c	15	740	16.3	183915	14	AC073967	AC073967 Homo sapi
	16	554	12.2	601	6	AX321326	AX321326 Sequence
c	17	394	8.7	5853	6	AX828539	AX828539 Sequence
c	18	393	8.7	393	6	AX828493	AX828493 Sequence
	19	331	7.3	331	6	AX321316	AX321316 Sequence
	20	322	7.1	2440	8	AB179164	AB179164 Macaca fa
c	21	310	6.8	172105	8	AC093135	AC093135 Pan trogl
c	22	310	6.8	199670	8	AC142303	AC142303 Pan trogl
c	23	310	6.8	221091	8	AC146228	AC146228 Pan trogl
	24	259	5.7	518	6	CQ102544	CQ102544 Sequence
	25	259	5.7	518	6	CQ141451	CQ141451 Sequence
	26	259	5.7	518	6	CQ224738	CQ224738 Sequence
	27	259	5.7	518	6	CQ299810	CQ299810 Sequence
	28	259	5.7	518	6	CQ336990	CQ336990 Sequence
c	29	250	5.5	166701	8	AC147785	AC147785 Pan trogl
	30	187	4.1	436	6	AR153645	AR153645 Sequence
	31	187	4.1	436	6	BD227056	BD227056 Apoptosis
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	33	184	4.1	184	6	CQ115605	CQ115605 Sequence
	34	184	4.1	184	6	CQ154394	CQ154394 Sequence
	35	184	4.1	184	6	CQ237647	CQ237647 Sequence
	36	184	4.1	184	6	CQ312242	CQ312242 Sequence
	37	184	4.1	184	6	CQ349660	CQ349660 Sequence
	38	175	3.9	279	6	AR153660	AR153660 Sequence
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	40	175	3.9	279	8	HSAHIPI27	AF052287 Homo sapi
c	41	163	3.6	1290	6	CQ742344	CQ742344 Sequence
	42	163	3.6	175839	8	AC004491	AC004491 Homo sapi
c	43	163	3.6	195646	8	AC093709	AC093709 Pan trogl
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c	45	161	3.6	243	10	G30915	G30915 sWSS3387 Er

ALIGNMENTS

RESULT 1
HSU79734
LOCUS   HSU79734   4714 bp   mRNA   linear   PRI 06-MAY-1997
DEFINITION Human huntingtin interacting protein (HIP1) mRNA, complete cds.
ACCESSION   U79734
VERSION   U79734.1 GI:2072422
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens

FEATURES   Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /note="putative orf; similar to SLA2 Saccharomyces
                     cerevisiae, encoded by Genbank Accession Number Z22811,
                     and ZK370.3 protein in Caenorhabditis elegans, encoded by
                     Genbank Accession Number M98552"
                     /codon_start=1
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                     /protein_id="AAC51257.1"
                     /db_xref="GI:2072423"
                     /translation="MSRMWGHLSEGYGQLCSIYLKLLRTKMEYHTKNPRFPGNLQMSD
                     RQLDEAGESDVNNFFQLTVEMFDYLECELNLFQTVFNSLDMSRSVSVTAAGQCRLAPL
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                     RLIQIPQLPENPPNFLRASALSEHISPVVVIPAEASSPDSEPVLEKDDLMDMDASQQN
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                     RVVLQLKGHVSELEADLAEQQHLRQQAADDCEFLRAELDELRRQREDTEKAQRSLSEI
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                     EMDSQVRVLELENELQKERQKLGELRKKHYELAGVAEGWEEGTEASPPTLQEVVTEKE
                     "
ORIGIN

      Query Match   66.9%;   Score 3035;   DB 8;   Length 4714;
      Best Local Similarity 99.9%;   Pred. No. 0;

Matches 3135;   Conservative   0;   Mismatches   2;   Indels   0;   Gaps   0;

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Qy    183 CAGCATCAATAAGGCCATTAATACGCAGGAAGTGGCTGTAAAGGAAAAACACGCCAGAAC 242
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Db      1 CAGCATCAATAAGGCCATTAATACGCAGGAAGTGGCTGTAAAGGAAAAACACGCCAGAAC 60

Qy    243 GTGCATACTGGGCACCCACCATGAGAAAGGGGCACAGACCTTCTGGTCTGTTGTCAACCG 302
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GTGCATACTGGGCACCCACCATGAGAAAGGGGCACAGACCTTCTGGTCTGTTGTCAACCG 120

Qy    303 CCTGCCTCTGTCTAGCAACGCAGTGCTCTGCTGGAAGTTCTGCCATGTGTTCCACAAACT 362
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Db    121 CCTGCCTCTGTCTAGCAACGCAGTGCTCTGCTGGAAGTTCTGCCATGTGTTCCACAAACT 180

Qy    363 CCTCCGAGATGGACACCCGAACGTCCTGAAGGACTCTCTGAGATACAGAAATGAATTGAG 422
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Db    181 CCTCCGAGATGGACACCCGAACGTCCTGAAGGACTCTCTGAGATACAGAAATGAATTGAG 240

Qy    423 TGACATGAGCAGGATGTGGGGCTACCTGAGCGAGGGGTATGGCCAGCTGTGCAGCATCTA 482
          ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db    241 TGACATGAGCAGGATGTGGGGCCACCTGAGCGAGGGGTATGGCCAGCTGTGCAGCATCTA 300

Qy    483 CCTGAAACTGCTAAGAACCAAGATGGAGTACCACACCAAAAATCCCAGGTTCCCAGGCAA 542
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Db    301 CCTGAAACTGCTAAGAACCAAGATGGAGTACCACACCAAAAATCCCAGGTTCCCAGGCAA 360

Qy    543 CCTGCAGATGAGTGACCGCCAGCTGGACGAGGCTGGAGAAAGTGACGTGAACAACTTTTC 602
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Db    361 CCTGCAGATGAGTGACCGCCAGCTGGACGAGGCTGGAGAAAGTGACGTGAACAACTTTTT 420

Qy    603 CCAGTTAACAGTGGAGATGTTTGACTACCTGGAGTGTGAACTCAACCTCTTCCAAACAGT 662
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Qy    663 ATTCAACTCCCTGGACATGTCCCGCTCTGTGTCCGTGACGGCAGCAGGGCAGTGCCGCCT 722
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Db    481 ATTCAACTCCCTGGACATGTCCCGCTCTGTGTCCGTGACGGCAGCAGGGCAGTGCCGCCT 540

Qy    723 CGCCCCGCTGATCCAGGTCATCTTGGACTGCAGCCACCTTTATGACTACACTGTCAAGCT 782
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CGCCCCGCTGATCCAGGTCATCTTGGACTGCAGCCACCTTTATGACTACACTGTCAAGCT 600

Qy    783 TCTCTTCAAACTCCACTCCTGCCTCCCAGCTGACACCCTGCAAGGCCACCGGGACCGCTT 842
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TCTCTTCAAACTCCACTCCTGCCTCCCAGCTGACACCCTGCAAGGCCACCGGGACCGCTT 660

Qy    843 CATGGAGCAGTTTACAAAGTTGAAAGATCTGTTCTACCGCTCCAGCAACCTGCAGTACTT 902
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Db    661 CATGGAGCAGTTTACAAAGTTGAAAGATCTGTTCTACCGCTCCAGCAACCTGCAGTACTT 720

Qy    903 CAAGCGGCTCATTCAGATCCCCCAGCTGCCTGAGAACCCACCCAACTTCCTGCGAGCCTC 962
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Db    721 CAAGCGGCTCATTCAGATCCCCCAGCTGCCTGAGAACCCACCCAACTTCCTGCGAGCCTC 780

Qy    963 AGCCCTGTCAGAACATATCAGCCCTGTGGTGGTGATCCCTGCAGAGGCCTCATCCCCCGA 1022
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Qy    1023  CAGCGAGCCAGTCCTAGAGAAGGATGACCTCATGGACATGGATGCCTCTCAGCAGAATTT  1082
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Qy    1083  ATTTGACAACAAGTTTGATGACATCTTTGGCAGTTCATTCAGCAGTGATCCCTTCAATTT  1142
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Db     901  ATTTGACAACAAGTTTGATGACATCTTTGGCAGTTCATTCAGCAGTGATCCCTTCAATTT   960

Qy    1143  CAACAGTCAAAATGGTGTGAACAAGGATGAGAAGGACCACTTAATTGAGCGACTATACAG  1202
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Db     961  CAACAGTCAAAATGGTGTGAACAAGGATGAGAAGGACCACTTAATTGAGCGACTATACAG  1020

Qy    1203  AGAGATCAGTGGATTGAAGGCACAGCTAGAAAACATGAAGACTGAGAGCCAGCGGGTTGT  1262
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Db    1021  AGAGATCAGTGGATTGAAGGCACAGCTAGAAAACATGAAGACTGAGAGCCAGCGGGTTGT  1080

Qy    1263  GCTGCAGCTGAAGGGCCACGTCAGCGAGCTGGAAGCAGATCTGGCCGAGCAGCAGCACCT  1322
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Qy    1323  GCGGCAGCAGGCGGCCGACGACTGTGAATTCCTGCGGGCAGAACTGGACGAGCTCAGGAG  1382
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Qy    1383  GCAGCGGGAGGACACCGAGAAGGCTCAGCGGAGCCTGTCTGAGATAGAAAGGAAAGCTCA  1442
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Qy    1443  AGCCAATGAACAGCGATATAGCAAGCTAAAGGAGAAGTACAGCGAGCTGGTTCAGAACCA  1502
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Qy    1683  TGCCACAAGCCAACGGGAGCTTCAGGTTCTGCAAGGCAGCCTGGAAACTTCTGCCCAGTC  1742
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Qy    1803  TGGCGCAGCTCATAGGGAGGAGGAATTATCTGCTCTTCGGAAAGAACTGCAGGACACTCA  1862
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Db    1621  TGGCGCAGCTCATAGGGAGGAGGAATTATCTGCTCTTCGGAAAGAACTGCAGGACACTCA  1680
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Qy   1863 GCTCAAACTGGCCAGCACAGAGGAATCTATGTGCCAGCTTGCCAAAGACCAACGAAAAAT 1922
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Db   1681 GCTCAAACTGGCCAGCACAGAGGAATCTATGTGCCAGCTTGCCAAAGACCAACGAAAAAT 1740

Qy   1923 GCTTCTGGTGGGGTCCAGGAAGGCTGCGGAGCAGGTGATACAAGACGCCCTGAACCAGCT 1982
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Qy   1983 TGAAGAACCTCCTCTCATCAGCTGCGCTGGGTCTGCAGATCACCTCCTCTCCACGGTCAC 2042
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Qy   2043 ATCCATTTCCAGCTGCATCGAGCAACTGGAGAAAAGCTGGAGCCAGTATCTGGCCTGCCC 2102
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Qy   2103 AGAAGACATCAGTGGACTTCTCCATTCCATAACCCTGCTGGCCCACTTGACCAGCGACGC 2162
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Qy   2163 CATTGCTCATGGTGCCACCACCTGCCTCAGAGCCCCACCTGAGCCTGCCGACTCACTGAC 2222
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Qy   2223 CGAGGCCTGTAAGCAGTATGGCAGGGAAACCCTCGCCTACCTGGCCTCCCTGGAGGAAGA 2282
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Qy   2343 CATCGGCGAGGAGCTCCTGCCCAGGGGACTGGACATCAAGCAGGAGGAGCTGGGGGACCT 2402
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Qy   2463 GGAGATGCTCAGCAAATCCCGAGCAGGAGACACAGGAGTCAAATTGGAGGTGAATGAAAG 2522
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Qy   2523 GATCCTTGGTTGCTGTACCAGCCTCATGCAAGCTATTCAGGTGCTCATCGTGGCCTCTAA 2582
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Qy   2583 GGACCTCCAGAGAGAGATTGTGGAGAGCGGCAGGGGTACAGCATCCCCTAAAGAGTTTTA 2642
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Qy   2643 TGCCAAGAACTCTCGATGGACAGAAGGACTTATCTCAGCCTCCAAGGCTGTGGGCTGGGG 2702
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Db   2461 TGCCAAGAACTCTCGATGGACAGAAGGACTTATCTCAGCCTCCAAGGCTGTGGGCTGGGG 2520

Qy   2703 AGCCACTGTCATGGTGGATGCAGCTGATCTGGTGGTACAAGGCAGAGGGAAATTTGAGGA 2762
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2521  AGCCACTGTCATGGTGGATGCAGCTGATCTGGTGGTACAAGGCAGAGGGAAATTTGAGGA 2580

Qy      2763  GCTAATGGTGTGTTCTCATGAAATTGCTGCTAGCACAGCCCAGCTTGTGGCTGCATCCAA 2822
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2581  GCTAATGGTGTGTTCTCATGAAATTGCTGCTAGCACAGCCCAGCTTGTGGCTGCATCCAA 2640

Qy      2823  GGTGAAAGCTGATAAGGACAGCCCCAACCTAGCCCAGCTGCAGCAGGCCTCTCGGGGAGT 2882
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Db      2641  GGTGAAAGCTGATAAGGACAGCCCCAACCTAGCCCAGCTGCAGCAGGCCTCTCGGGGAGT 2700

Qy      2883  GAACCAGGCCACTGCCGGCGTTGTGGCCTCAACCATTTCCGGCAAATCACAGATCGAAGA 2942
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Db      2701  GAACCAGGCCACTGCCGGCGTTGTGGCCTCAACCATTTCCGGCAAATCACAGATCGAAGA 2760

Qy      2943  GACAGACAACATGGACTTCTCAAGCATGACGCTGACACAGATCAAACGCCAAGAGATGGA 3002
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2761  GACAGACAACATGGACTTCTCAAGCATGACGCTGACACAGATCAAACGCCAAGAGATGGA 2820

Qy      3003  TTCTCAGGTTAGGGTGCTAGAGCTAGAAAATGAATTGCAGAAGGAGCGTCAAAAACTGGG 3062
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2821  TTCTCAGGTTAGGGTGCTAGAGCTAGAAAATGAATTGCAGAAGGAGCGTCAAAAACTGGG 2880

Qy      3063  AGAGCTTCGGAAAAAGCACTACGAGCTTGCTGGTGTTGCTGAGGGCTGGGAAGAAGGAAC 3122
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Db      2881  AGAGCTTCGGAAAAAGCACTACGAGCTTGCTGGTGTTGCTGAGGGCTGGGAAGAAGGAAC 2940

Qy      3123  AGAGGCATCTCCACCTACACTGCAAGAAGTGGTAACCGAAAAAGAATAGAGCCAAACCAA 3182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2941  AGAGGCATCTCCACCTACACTGCAAGAAGTGGTAACCGAAAAAGAATAGAGCCAAACCAA 3000

Qy      3183  CACCCCATATGTCAGTGTAAATCCTTGTTACCTATCTCGTGTGTGTTATTTCCCCAGCCA 3242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3001  CACCCCATATGTCAGTGTAAATCCTTGTTACCTATCTCGTGTGTGTTATTTCCCCAGCCA 3060

Qy      3243  CAGGCCAAATCCTTGGAGTCCCAGGGGCAGCCACACCACTGCCATTACCCAGTGCCGAGG 3302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3061  CAGGCCAAATCCTTGGAGTCCCAGGGGCAGCCACACCACTGCCATTACCCAGTGCCGAGG 3120

Qy      3303  ACATGCATGACACTTCC 3319
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Db      3121  ACATGCATGACACTTCC 3137
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RESULT 2
AX828392
LOCUS   AX828392   6626 bp   DNA   linear   PAT 12-DEC-2003
DEFINITION Sequence 38 from Patent WO03074073.
ACCESSION   AX828392
VERSION   AX828392.1 GI:39838392
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1

FEATURES   Location/Qualifiers
     source   1. .6626
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"
ORIGIN

   Query Match   66.9%; Score 3035; DB 6; Length 6626;
   Best Local Similarity   99.9%; Pred. No. 0;
   Matches 3135; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

Qy   183 CAGCATCAATAAGGCCATTAATACGCAGGAAGTGGCTGTAAAGGAAAAACACGCCAGAAC 242
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CAGCATCAATAAGGCCATTAATACGCAGGAAGTGGCTGTAAAGGAAAAACACGCCAGAAC 60

Qy   243 GTGCATACTGGGCACCCACCATGAGAAAGGGGCACAGACCTTCTGGTCTGTTGTCAACCG 302
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GTGCATACTGGGCACCCACCATGAGAAAGGGGCACAGACCTTCTGGTCTGTTGTCAACCG 120

Qy   303 CCTGCCTCTGTCTAGCAACGCAGTGCTCTGCTGGAAGTTCTGCCATGTGTTCCACAAACT 362
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CCTGCCTCTGTCTAGCAACGCAGTGCTCTGCTGGAAGTTCTGCCATGTGTTCCACAAACT 180

Qy   363 CCTCCGAGATGGACACCCGAACGTCCTGAAGGACTCTCTGAGATACAGAAATGAATTGAG 422
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CCTCCGAGATGGACACCCGAACGTCCTGAAGGACTCTCTGAGATACAGAAATGAATTGAG 240

Qy   423 TGACATGAGCAGGATGTGGGGCTACCTGAGCGAGGGGTATGGCCAGCTGTGCAGCATCTA 482
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db   241 TGACATGAGCAGGATGTGGGGCCACCTGAGCGAGGGGTATGGCCAGCTGTGCAGCATCTA 300

Qy   483 CCTGAAACTGCTAAGAACCAAGATGGAGTACCACACCAAAAATCCCAGGTTCCCAGGCAA 542
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CCTGAAACTGCTAAGAACCAAGATGGAGTACCACACCAAAAATCCCAGGTTCCCAGGCAA 360

Qy   543 CCTGCAGATGAGTGACCGCCAGCTGGACGAGGCTGGAGAAAGTGACGTGAACAACTTTTC 602
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CCTGCAGATGAGTGACCGCCAGCTGGACGAGGCTGGAGAAAGTGACGTGAACAACTTTTT 420

Qy   603 CCAGTTAACAGTGGAGATGTTTGACTACCTGGAGTGTGAACTCAACCTCTTCCAAACAGT 662
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 CCAGTTAACAGTGGAGATGTTTGACTACCTGGAGTGTGAACTCAACCTCTTCCAAACAGT 480

Qy   663 ATTCAACTCCCTGGACATGTCCCGCTCTGTGTCCGTGACGGCAGCAGGGCAGTGCCGCCT 722
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   481 ATTCAACTCCCTGGACATGTCCCGCTCTGTGTCCGTGACGGCAGCAGGGCAGTGCCGCCT 540

Qy   723 CGCCCCGCTGATCCAGGTCATCTTGGACTGCAGCCACCTTTATGACTACACTGTCAAGCT 782
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   541 CGCCCCGCTGATCCAGGTCATCTTGGACTGCAGCCACCTTTATGACTACACTGTCAAGCT 600

Qy   783 TCTCTTCAAACTCCACTCCTGCCTCCCAGCTGACACCCTGCAAGGCCACCGGGACCGCTT 842

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            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601   TCTCTTCAAACTCCACTCCTGCCTCCCAGCTGACACCCTGCAAGGCCACCGGGACCGCTT 660

Qy    843   CATGGAGCAGTTTACAAAGTTGAAAGATCTGTTCTACCGCTCCAGCAACCTGCAGTACTT 902
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661   CATGGAGCAGTTTACAAAGTTGAAAGATCTGTTCTACCGCTCCAGCAACCTGCAGTACTT 720

Qy    903   CAAGCGGCTCATTCAGATCCCCCAGCTGCCTGAGAACCCACCCAACTTCCTGCGAGCCTC 962
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721   CAAGCGGCTCATTCAGATCCCCCAGCTGCCTGAGAACCCACCCAACTTCCTGCGAGCCTC 780

Qy    963   AGCCCTGTCAGAACATATCAGCCCTGTGGTGGTGATCCCTGCAGAGGCCTCATCCCCCGA 1022
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781   AGCCCTGTCAGAACATATCAGCCCTGTGGTGGTGATCCCTGCAGAGGCCTCATCCCCCGA 840

Qy    1023  CAGCGAGCCAGTCCTAGAGAAGGATGACCTCATGGACATGGATGCCTCTCAGCAGAATTT 1082
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841   CAGCGAGCCAGTCCTAGAGAAGGATGACCTCATGGACATGGATGCCTCTCAGCAGAATTT 900

Qy    1083  ATTTGACAACAAGTTTGATGACATCTTTGGCAGTTCATTCAGCAGTGATCCCTTCAATTT 1142
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901   ATTTGACAACAAGTTTGATGACATCTTTGGCAGTTCATTCAGCAGTGATCCCTTCAATTT 960

Qy    1143  CAACAGTCAAAATGGTGTGAACAAGGATGAGAAGGACCACTTAATTGAGCGACTATACAG 1202
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961   CAACAGTCAAAATGGTGTGAACAAGGATGAGAAGGACCACTTAATTGAGCGACTATACAG 1020

Qy    1203  AGAGATCAGTGGATTGAAGGCACAGCTAGAAAACATGAAGACTGAGAGCCAGCGGGTTGT 1262
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021  AGAGATCAGTGGATTGAAGGCACAGCTAGAAAACATGAAGACTGAGAGCCAGCGGGTTGT 1080

Qy    1263  GCTGCAGCTGAAGGGCCACGTCAGCGAGCTGGAAGCAGATCTGGCCGAGCAGCAGCACCT 1322
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081  GCTGCAGCTGAAGGGCCACGTCAGCGAGCTGGAAGCAGATCTGGCCGAGCAGCAGCACCT 1140

Qy    1323  GCGGCAGCAGGCGGCCGACGACTGTGAATTCCTGCGGGCAGAACTGGACGAGCTCAGGAG 1382
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141  GCGGCAGCAGGCGGCCGACGACTGTGAATTCCTGCGGGCAGAACTGGACGAGCTCAGGAG 1200

Qy    1383  GCAGCGGGAGGACACCGAGAAGGCTCAGCGGAGCCTGTCTGAGATAGAAAGGAAAGCTCA 1442
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201  GCAGCGGGAGGACACCGAGAAGGCTCAGCGGAGCCTGTCTGAGATAGAAAGGAAAGCTCA 1260

Qy    1443  AGCCAATGAACAGCGATATAGCAAGCTAAAGGAGAAGTACAGCGAGCTGGTTCAGAACCA 1502
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261  AGCCAATGAACAGCGATATAGCAAGCTAAAGGAGAAGTACAGCGAGCTGGTTCAGAACCA 1320

Qy    1503  CGCTGACCTGCTGCGGAAGAATGCAGAGGTGACCAAACAGGTGTCCATGGCCAGACAAGC 1562
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321  CGCTGACCTGCTGCGGAAGAATGCAGAGGTGACCAAACAGGTGTCCATGGCCAGACAAGC 1380

Qy    1563  CCAGGTAGATTTGGAACGAGAGAAAAAAGAGCTGGAGGATTCGTTGGAGCGCATCAGTGA 1622
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381  CCAGGTAGATTTGGAACGAGAGAAAAAAGAGCTGGAGGATTCGTTGGAGCGCATCAGTGA 1440

Qy    1623  CCAGGGCCAGCGGAAGACTCAAGAACAGCTGGAAGTTCTAGAGAGCTTGAAGCAGGAACT 1682
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db    1441 CCAGGGCCAGCGGAAGACTCAAGAACAGCTGGAAGTTCTAGAGAGCTTGAAGCAGGAACT 1500

Qy    1683 TGCCACAAGCCAACGGGAGCTTCAGGTTCTGCAAGGCAGCCTGGAAACTTCTGCCCAGTC 1742
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 TGCCACAAGCCAACGGGAGCTTCAGGTTCTGCAAGGCAGCCTGGAAACTTCTGCCCAGTC 1560

Qy    1743 AGAAGCAAACTGGGCAGCCGAGTTCGCCGAGCTAGAGAAGGAGCGGGACAGCCTGGTGAG 1802
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 AGAAGCAAACTGGGCAGCCGAGTTCGCCGAGCTAGAGAAGGAGCGGGACAGCCTGGTGAG 1620

Qy    1803 TGGCGCAGCTCATAGGGAGGAGGAATTATCTGCTCTTCGGAAAGAACTGCAGGACACTCA 1862
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 TGGCGCAGCTCATAGGGAGGAGGAATTATCTGCTCTTCGGAAAGAACTGCAGGACACTCA 1680

Qy    1863 GCTCAAACTGGCCAGCACAGAGGAATCTATGTGCCAGCTTGCCAAAGACCAACGAAAAAT 1922
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 GCTCAAACTGGCCAGCACAGAGGAATCTATGTGCCAGCTTGCCAAAGACCAACGAAAAAT 1740

Qy    1923 GCTTCTGGTGGGGTCCAGGAAGGCTGCGGAGCAGGTGATACAAGACGCCCTGAACCAGCT 1982
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 GCTTCTGGTGGGGTCCAGGAAGGCTGCGGAGCAGGTGATACAAGACGCCCTGAACCAGCT 1800

Qy    1983 TGAAGAACCTCCTCTCATCAGCTGCGCTGGGTCTGCAGATCACCTCCTCTCCACGGTCAC 2042
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801 TGAAGAACCTCCTCTCATCAGCTGCGCTGGGTCTGCAGATCACCTCCTCTCCACGGTCAC 1860

Qy    2043 ATCCATTTCCAGCTGCATCGAGCAACTGGAGAAAAGCTGGAGCCAGTATCTGGCCTGCCC 2102
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861 ATCCATTTCCAGCTGCATCGAGCAACTGGAGAAAAGCTGGAGCCAGTATCTGGCCTGCCC 1920

Qy    2103 AGAAGACATCAGTGGACTTCTCCATTCCATAACCCTGCTGGCCCACTTGACCAGCGACGC 2162
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921 AGAAGACATCAGTGGACTTCTCCATTCCATAACCCTGCTGGCCCACTTGACCAGCGACGC 1980

Qy    2163 CATTGCTCATGGTGCCACCACCTGCCTCAGAGCCCCACCTGAGCCTGCCGACTCACTGAC 2222
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1981 CATTGCTCATGGTGCCACCACCTGCCTCAGAGCCCCACCTGAGCCTGCCGACTCACTGAC 2040

Qy    2223 CGAGGCCTGTAAGCAGTATGGCAGGGAAACCCTCGCCTACCTGGCCTCCCTGGAGGAAGA 2282
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Db    2041 CGAGGCCTGTAAGCAGTATGGCAGGGAAACCCTCGCCTACCTGGCCTCCCTGGAGGAAGA 2100

Qy    2283 GGGAAGCCTTGAGAATGCCGACAGCACAGCCATGAGGAACTGCCTGAGCAAGATCAAGGC 2342
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Qy    2343 CATCGGCGAGGAGCTCCTGCCCAGGGGACTGGACATCAAGCAGGAGGAGCTGGGGGACCT 2402
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Db    2161 CATCGGCGAGGAGCTCCTGCCCAGGGGACTGGACATCAAGCAGGAGGAGCTGGGGGACCT 2220

Qy    2403 GGTGGACAAGGAGATGGCGGCCACTTCAGCTGCTATTGAAACTGCCACGGCCAGAATAGA 2462
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2221 GGTGGACAAGGAGATGGCGGCCACTTCAGCTGCTATTGAAACTGCCACGGCCAGAATAGA 2280

Qy    2463 GGAGATGCTCAGCAAATCCCGAGCAGGAGACACAGGAGTCAAATTGGAGGTGAATGAAAG 2522
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2281 GGAGATGCTCAGCAAATCCCGAGCAGGAGACACAGGAGTCAAATTGGAGGTGAATGAAAG 2340
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Qy   2523 GATCCTTGGTTGCTGTACCAGCCTCATGCAAGCTATTCAGGTGCTCATCGTGGCCTCTAA 2582
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Db   2341 GATCCTTGGTTGCTGTACCAGCCTCATGCAAGCTATTCAGGTGCTCATCGTGGCCTCTAA 2400

Qy   2583 GGACCTCCAGAGAGAGATTGTGGAGAGCGGCAGGGGTACAGCATCCCCTAAAGAGTTTTA 2642
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 GGACCTCCAGAGAGAGATTGTGGAGAGCGGCAGGGGTACAGCATCCCCTAAAGAGTTTTA 2460

Qy   2643 TGCCAAGAACTCTCGATGGACAGAAGGACTTATCTCAGCCTCCAAGGCTGTGGGCTGGGG 2702
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Db   2461 TGCCAAGAACTCTCGATGGACAGAAGGACTTATCTCAGCCTCCAAGGCTGTGGGCTGGGG 2520

Qy   2703 AGCCACTGTCATGGTGGATGCAGCTGATCTGGTGGTACAAGGCAGAGGGAAATTTGAGGA 2762
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Qy   2763 GCTAATGGTGTGTTCTCATGAAATTGCTGCTAGCACAGCCCAGCTTGTGGCTGCATCCAA 2822
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Qy   2823 GGTGAAAGCTGATAAGGACAGCCCCAACCTAGCCCAGCTGCAGCAGGCCTCTCGGGGAGT 2882
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Qy   2883 GAACCAGGCCACTGCCGGCGTTGTGGCCTCAACCATTTCCGGCAAATCACAGATCGAAGA 2942
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Qy   2943 GACAGACAACATGGACTTCTCAAGCATGACGCTGACACAGATCAAACGCCAAGAGATGGA 3002
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 GACAGACAACATGGACTTCTCAAGCATGACGCTGACACAGATCAAACGCCAAGAGATGGA 2820

Qy   3003 TTCTCAGGTTAGGGTGCTAGAGCTAGAAAATGAATTGCAGAAGGAGCGTCAAAAACTGGG 3062
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Qy   3063 AGAGCTTCGGAAAAAGCACTACGAGCTTGCTGGTGTTGCTGAGGGCTGGGAAGAAGGAAC 3122
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   3123 AGAGGCATCTCCACCTACACTGCAAGAAGTGGTAACCGAAAAAGAATAGAGCCAAACCAA 3182
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 AGAGGCATCTCCACCTACACTGCAAGAAGTGGTAACCGAAAAAGAATAGAGCCAAACCAA 3000

Qy   3183 CACCCCATATGTCAGTGTAAATCCTTGTTACCTATCTCGTGTGTGTTATTTCCCCAGCCA 3242
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 CACCCCATATGTCAGTGTAAATCCTTGTTACCTATCTCGTGTGTGTTATTTCCCCAGCCA 3060

Qy   3243 CAGGCCAAATCCTTGGAGTCCCAGGGGCAGCCACACCACTGCCATTACCCAGTGCCGAGG 3302
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 CAGGCCAAATCCTTGGAGTCCCAGGGGCAGCCACACCACTGCCATTACCCAGTGCCGAGG 3120

Qy   3303 ACATGCATGACACTTCC 3319
          |||||||||||||||||
Db   3121 ACATGCATGACACTTCC 3137
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RESULT 3
CQ728008
LOCUS   CQ728008   4707 bp   DNA   linear   PAT 03-FEB-2004
DEFINITION   Sequence 13942 from Patent WO02068579.
ACCESSION   CQ728008
VERSION   CQ728008.1 GI:42295624
KEYWORDS   .
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE   Kits, such as nucleic acid arrays, comprising a majority of
             humanexons or transcripts, for detecting expression and other uses
             thereof
  JOURNAL   Patent: WO 02068579-A 13942 06-SEP-2002;
             PE Corporation (NY) (US)
FEATURES   Location/Qualifiers
     source   1. .4707
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

     Query Match   66.8%; Score 3028; DB 6; Length 4707;
     Best Local Similarity   99.9%; Pred. No. 0;
     Matches 3178; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

Qy   183 CAGCATCAATAAGGCCATTAATACGCAGGAAGTGGCTGTAAAGGAAAAACACGCCAGAAC 242
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 CAGCATCAATAAGGCCATTAATACGCAGGAAGTGGCTGTAAAGGAAAAACACGCCAGAAC 60

Qy   243 GTGCATACTGGGCACCCACCATGAGAAAGGGGCACAGACCTTCTGGTCTGTTGTCAACCG 302
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 GTGCATACTGGGCACCCACCATGAGAAAGGGGCACAGACCTTCTGGTCTGTTGTCAACCG 120

Qy   303 CCTGCCTCTGTCTAGCAACGCAGTGCTCTGCTGGAAGTTCTGCCATGTGTTCCACAAACT 362
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 CCTGCCTCTGTCTAGCAACGCAGTGCTCTGCTGGAAGTTCTGCCATGTGTTCCACAAACT 180

Qy   363 CCTCCGAGATGGACACCCGAACGTCCTGAAGGACTCTCTGAGATACAGAAATGAATTGAG 422
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CCTCCGAGATGGACACCCGAACGTCCTGAAGGACTCTCTGAGATACAGAAATGAATTGAG 240

Qy   423 TGACATGAGCAGGATGTGGGGCTACCTGAGCGAGGGGTATGGCCAGCTGTGCAGCATCTA 482
             ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db   241 TGACATGAGCAGGATGTGGGGCCACCTGAGCGAGGGGTATGGCCAGCTGTGCAGCATCTA 300

Qy   483 CCTGAAACTGCTAAGAACCAAGATGGAGTACCACACCAAAAATCCCAGGTTCCCAGGCAA 542
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 CCTGAAACTGCTAAGAACCAAGATGGAGTACCACACCAAAAATCCCAGGTTCCCAGGCAA 360

Qy   543 CCTGCAGATGAGTGACCGCCAGCTGGACGAGGCTGGAGAAAGTGACGTGAACAACTTTTC 602
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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Db    361 CCTGCAGATGAGTGACCGCCAGCTGGACGAGGCTGGAGAAAGTGACGTGAACAACTTTTT 420

Qy    603 CCAGTTAACAGTGGAGATGTTTGACTACCTGGAGTGTGAACTCAACCTCTTCCAAACAGT 662
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CCAGTTAACAGTGGAGATGTTTGACTACCTGGAGTGTGAACTCAACCTCTTCCAAACAGT 480

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Db    481 ATTCAACTCCCTGGACATGTCCCGCTCTGTGTCCGTGACGGCAGCAGGGCAGTGCCGCCT 540

Qy    723 CGCCCCGCTGATCCAGGTCATCTTGGACTGCAGCCACCTTTATGACTACACTGTCAAGCT 782
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 CGCCCCGCTGATCCAGGTCATCTTGGACTGCAGCCACCTTTATGACTACACTGTCAAGCT 600

Qy    783 TCTCTTCAAACTCCACTCCTGCCTCCCAGCTGACACCCTGCAAGGCCACCGGGACCGCTT 842
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 TCTCTTCAAACTCCACTCCTGCCTCCCAGCTGACACCCTGCAAGGCCACCGGGACCGCTT 660

Qy    843 CATGGAGCAGTTTACAAAGTTGAAAGATCTGTTCTACCGCTCCAGCAACCTGCAGTACTT 902
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CATGGAGCAGTTTACAAAGTTGAAAGATCTGTTCTACCGCTCCAGCAACCTGCAGTACTT 720

Qy    903 CAAGCGGCTCATTCAGATCCCCCAGCTGCCTGAGAACCCACCCAACTTCCTGCGAGCCTC 962
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CAAGCGGCTCATTCAGATCCCCCAGCTGCCTGAGAACCCACCCAACTTCCTGCGAGCCTC 780

Qy    963 AGCCCTGTCAGAACATATCAGCCCTGTGGTGGTGATCCCTGCAGAGGCCTCATCCCCCGA 1022
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 AGCCCTGTCAGAACATATCAGCCCTGTGGTGGTGATCCCTGCAGAGGCCTCATCCCCCGA 840

Qy   1023 CAGCGAGCCAGTCCTAGAGAAGGATGACCTCATGGACATGGATGCCTCTCAGCAGAATTT 1082
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 CAGCGAGCCAGTCCTAGAGAAGGATGACCTCATGGACATGGATGCCTCTCAGCAGAATTT 900

Qy   1083 ATTTGACAACAAGTTTGATGACATCTTTGGCAGTTCATTCAGCAGTGATCCCTTCAATTT 1142
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 ATTTGACAACAAGTTTGATGACATCTTTGGCAGTTCATTCAGCAGTGATCCCTTCAATTT 960

Qy   1143 CAACAGTCAAAATGGTGTGAACAAGGATGAGAAGGACCACTTAATTGAGCGACTATACAG 1202
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 CAACAGTCAAAATGGTGTGAACAAGGATGAGAAGGACCACTTAATTGAGCGACTATACAG 1020

Qy   1203 AGAGATCAGTGGATTGAAGGCACAGCTAGAAAACATGAAGACTGAGAGCCAGCGGGTTGT 1262
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 AGAGATCAGTGGATTGAAGGCACAGCTAGAAAACATGAAGACTGAGAGCCAGCGGGTTGT 1080

Qy   1263 GCTGCAGCTGAAGGGCCACGTCAGCGAGCTGGAAGCAGATCTGGCCGAGCAGCAGCACCT 1322
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Db   1081 GCTGCAGCTGAAGGGCCACGTCAGCGAGCTGGAAGCAGATCTGGCCGAGCAGCAGCACCT 1140

Qy   1323 GCGGCAGCAGGCGGCCGACGACTGTGAATTCCTGCGGGCAGAACTGGACGAGCTCAGGAG 1382
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Db   1141 GCGGCAGCAGGCGGCCGACGACTGTGAATTCCTGCGGGCAGAACTGGACGAGCTCAGGAG 1200

Qy   1383 GCAGCGGGAGGACACCGAGAAGGCTCAGCGGAGCCTGTCTGAGATAGAAAGGAAAGCTCA 1442
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 GCAGCGGGAGGACACCGAGAAGGCTCAGCGGAGCCTGTCTGAGATAGAAAGGAAAGCTCA 1260
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Qy    1443 AGCCAATGAACAGCGATATAGCAAGCTAAAGGAGAAGTACAGCGAGCTGGTTCAGAACCA 1502
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Qy    1503 CGCTGACCTGCTGCGGAAGAATGCAGAGGTGACCAAACAGGTGTCCATGGCCAGACAAGC 1562
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Qy    1563 CCAGGTAGATTTGGAACGAGAGAAAAAGAGCTGGAGGATTCGTTGGAGCGCATCAGTGA 1622
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Db    1381 CCAGGTAGATTTGGAACGAGAGAAAAAGAGCTGGAGGATTCGTTGGAGCGCATCAGTGA 1440

Qy    1623 CCAGGGCCAGCGGAAGACTCAAGAACAGCTGGAAGTTCTAGAGAGCTTGAAGCAGGAACT 1682
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Qy    1683 TGCCACAAGCCAACGGGAGCTTCAGGTTCTGCAAGGCAGCCTGGAAACTTCTGCCCAGTC 1742
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Db    1501 TGCCACAAGCCAACGGGAGCTTCAGGTTCTGCAAGGCAGCCTGGAAACTTCTGCCCAGTC 1560

Qy    1743 AGAAGCAAACTGGGCAGCCGAGTTCGCCGAGCTAGAGAAGGAGCGGGACAGCCTGGTGAG 1802
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Db    1561 AGAAGCAAACTGGGCAGCCGAGTTCGCCGAGCTAGAGAAGGAGCGGGACAGCCTGGTGAG 1620

Qy    1803 TGGCGCAGCTCATAGGGAGGAGGAATTATCTGCTCTTCGGAAAGAACTGCAGGACACTCA 1862
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621 TGGCGCAGCTCATAGGGAGGAGGAATTATCTGCTCTTCGGAAAGAACTGCAGGACACTCA 1680

Qy    1863 GCTCAAACTGGCCAGCACAGAGGAATCTATGTGCCAGCTTGCCAAAGACCAACGAAAAAT 1922
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681 GCTCAAACTGGCCAGCACAGAGGAATCTATGTGCCAGCTTGCCAAAGACCAACGAAAAAT 1740

Qy    1923 GCTTCTGGTGGGGTCCAGGAAGGCTGCGGAGCAGGTGATACAAGACGCCCTGAACCAGCT 1982
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741 GCTTCTGGTGGGGTCCAGGAAGGCTGCGGAGCAGGTGATACAAGACGCCCTGAACCAGCT 1800

Qy    1983 TGAAGAACCTCCTCTCATCAGCTGCGCTGGGTCTGCAGATCACCTCCTCTCCACGGTCAC 2042
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Db    1801 TGAAGAACCTCCTCTCATCAGCTGCGCTGGGTCTGCAGATCACCTCCTCTCCACGGTCAC 1860

Qy    2043 ATCCATTTCCAGCTGCATCGAGCAACTGGAGAAAAGCTGGAGCCAGTATCTGGCCTGCCC 2102
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Qy    2103 AGAAGACATCAGTGGACTTCTCCATTCCATAACCCTGCTGGCCCACTTGACCAGCGACGC 2162
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Db    1921 AGAAGACATCAGTGGACTTCTCCATTCCATAACCCTGCTGGCCCACTTGACCAGCGACGC 1980

Qy    2163 CATTGCTCATGGTGCCACCACCTGCCTCAGAGCCCCACCTGAGCCTGCCGACTCACTGAC 2222
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Qy    2223 CGAGGCCTGTAAGCAGTATGGCAGGGAAACCCTCGCCTACCTGGCCTCCCTGGAGGAAGA 2282
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Db    2041 CGAGGCCTGTAAGCAGTATGGCAGGGAAACCCTCGCCTACCTGGCCTCCCTGGAGGAAGA 2100
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Qy   2283 GGGAAGCCTTGAGAATGCCGACAGCACAGCCATGAGGAACTGCCTGAGCAAGATCAAGGC 2342
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 GGGAAGCCTTGAGAATGCCGACAGCACAGCCATGAGGAACTGCCTGAGCAAGATCAAGGC 2160

Qy   2343 CATCGGCGAGGAGCTCCTGCCCAGGGGACTGGACATCAAGCAGGAGGAGCTGGGGGACCT 2402
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   2403 GGTGGACAAGGAGATGGCGGCCACTTCAGCTGCTATTGAAACTGCCACGGCCAGAATAGA 2462
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 GGTGGACAAGGAGATGGCGGCCACTTCAGCTGCTATTGAAACTGCCACGGCCAGAATAGA 2280

Qy   2463 GGAGATGCTCAGCAAATCCCGAGCAGGAGACACAGGAGTCAAATTGGAGGTGAATGAAAG 2522
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 GGAGATGCTCAGCAAATCCCGAGCAGGAGACACAGGAGTCAAATTGGAGGTGAATGAAAG 2340

Qy   2523 GATCCTTGGTTGCTGTACCAGCCTCATGCAAGCTATTCAGGTGCTCATCGTGGCCTCTAA 2582
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 GATCCTTGGTTGCTGTACCAGCCTCATGCAAGCTATTCAGGTGCTCATCGTGGCCTCTAA 2400

Qy   2583 GGACCTCCAGAGAGAGATTGTGGAGAGCGGCAGGGGTACAGCATCCCCTAAAGAGTTTTA 2642
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Db   2401 GGACCTCCAGAGAGAGATTGTGGAGAGCGGCAGGGGTACAGCATCCCCTAAAGAGTTTTA 2460

Qy   2643 TGCCAAGAACTCTCGATGGACAGAAGGACTTATCTCAGCCTCCAAGGCTGTGGGCTGGGG 2702
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Db   2461 TGCCAAGAACTCTCGATGGACAGAAGGACTTATCTCAGCCTCCAAGGCTGTGGGCTGGGG 2520

Qy   2703 AGCCACTGTCATGGTGGATGCAGCTGATCTGGTGGTACAAGGCAGAGGGAAATTTGAGGA 2762
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Db   2521 AGCCACTGTCATGGTGGATGCAGCTGATCTGGTGGTACAAGGCAGAGGGAAATTTGAGGA 2580

Qy   2763 GCTAATGGTGTGTTCTCATGAAATTGCTGCTAGCACAGCCCAGCTTGTGGCTGCATCCAA 2822
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Qy   2823 GGTGAAAGCTGATAAGGACAGCCCCAACCTAGCCCAGCTGCAGCAGGCCTCTCGGGGAGT 2882
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Db   2641 GGTGAAAGCTGATAAGGACAGCCCCTAACCTAGCCCAGCTGCAGCAGGCCTCTCGGGGAGT 2700

Qy   2883 GAACCAGGCCACTGCCGGCGTTGTGGCCTCAACCATTTCCGGCAAATCACAGATCGAAGA 2942
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Db   2701 GAACCAGGCCACTGCCGGCGTTGTGGCCTCAACCATTTCCGGCAAATCACAGATCGAAGA 2760

Qy   2943 GACAGACAACATGGACTTCTCAAGCATGACGCTGACACAGATCAAACGCCAAGAGATGGA 3002
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Db   2761 GACAGACAACATGGACTTCTCAAGCATGACGCTGACACAGATCAAACGCCAAGAGATGGA 2820

Qy   3003 TTCTCAGGTTAGGGTGCTAGAGCTAGAAAATGAATTGCAGAAGGAGCGTCAAAAACTGGG 3062
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Db   2821 TTCTCAGGTTAGGGTGCTAGAGCTAGAAAATGAATTGCAGAAGGAGCGTCAAAAACTGGG 2880

Qy   3063 AGAGCTTCGGAAAAAGCACTACGAGCTTGCTGGTGTTGCTGAGGGCTGGGAAGAAGGAAC 3122
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Db   2881 AGAGCTTCGGAAAAAGCACTACGAGCTTGCTGGTGTTGCTGAGGGCTGGGAAGAAGGAAC 2940

Qy   3123 AGAGGCATCTCCACCTACACTGCAAGAAGTGGTAACCGAAAAAGAATAGAGCCAAACCAA 3182
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Db   . 2941 AGAGGCATCTCCACCTACACTGCAAGAAGTGGTAACCGAAAAAGAATAGAGCCAAACCAA 3000

Qy    3183 CACCCCATATGTCAGTGTAAATCCTTGTTACCTATCTCGTGTGTGTTATTTCCCCAGCCA 3242
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3001 CACCCCATATGTCAGTGTAAATCCTTGTTACCTATCTCGTGTGTGTTATTTCCCCAGCCA 3060

Qy    3243 CAGGCCAAATCCTTGGAGTCCCAGGGGCAGCCACACCACTGCCATTACCCAGTGCCGAGG 3302
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3061 CAGGCCAAATCCTTGGAGTCCCAGGGGCAGCCACACCACTGCCATTACCCAGTGCCGAGG 3120

Qy    3303 ACATGCATGACACTTCCAAAGACTCCCTCCATAGCGACACCCTTTCTGTTTGGACCCATG 3362
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3121 ACATGCATGACACTTCCAAAGACTCCCTCCATAGCGACACCCTTTCTGTTTGGACCCATG 3180

Qy    3363 G 3363
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Db    3181 G 3181
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 07:57:30 ; Search time 1667 Seconds
                                    (without alignments)
                                    18127.004 Million cell updates/sec

Title: US-10-007-047-1
Perfect score: 4534
Sequence: 1 ccaagcttggtaccccggg..........gcatgcnntagagggcccta 4534

Scoring table: OLIGO_NUC
                  Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word size :   0

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   N_Geneseq_21:*
                  1: geneseqn1980s:*
                  2: geneseqn1990s:*
                  3: geneseqn2000s:*
                  4: geneseqn2001as:*
                  5: geneseqn2001bs:*
                  6: geneseqn2002as:*
                  7: geneseqn2002bs:*
                  8: geneseqn2003as:*
                  9: geneseqn2003bs:*

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            10:  geneseqn2003cs:*
            11:  geneseqn2003ds:*
            12:  geneseqn2004as:*
            13:  geneseqn2004bs:*
            14:  geneseqn2005s:*


     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.


                                      SUMMARIES
                        %
        Result        Query
           No.  Score  Match Length DB   ID                      Description
        ----------------------------------------------------------------------------
             1   4534  100.0   4534  10  ACC85533            Acc85533 Human HIP
             2   4534  100.0   4534  14  AEB71165            Aeb71165 DNA encod
             3   3911   86.3   3911  10  ACC85534            Acc85534 Human HIP
             4   3911   86.3   3911  14  AEB71167            Aeb71167 DNA encod
             5   3079   67.9   6623  13  ACN38651            Acn38651 Tumour-as
             6   3079   67.9   6624  13  ADQ86162            Adq86162 Human tum
             7   3035   66.9   6626  12  ADK60463            Adk60463 Angiogene
             8   3035   66.9   6626  12  ADK60764            Adk60764 Angiogene
             9   3035   66.9   6626  12  ADN01766            Adn01766 Human hun
            10   3035   66.9   6626  12  ADP73086            Adp73086 Angiogene
            11   3035   66.9   6626  13  ADP23862            Adp23862 PRO polyp
            12   2675   59.0   2745  14  ADV42966            Adv42966 Human psy
            13   2619   57.8   4796   2  AAT67187            Aat67187 Huntingti
            14   2619   57.8   4796   3  AAZ58746            Aaz58746 Human hun
            15   1160   25.6   1173  14  ADV77138            Adv77138 Huntingto
            16    973   21.5  65454  12  ADN01773            Adn01773 Human hun
            17    955   21.1   3715   3  AAZ58781            Aaz58781 Human HIP
            18    907   20.0   1164   2  AAT67186            Aat67186 Huntingti
            19    907   20.0   1164   3  AAZ58745            Aaz58745 Human hun
            20    554   12.2    601   6  AAS61792            Aas61792 Lung smal
     c      21    394    8.7   5853  12  ADK60309            Adk60309 Angiogene
     c      22    394    8.7   5853  12  ADK60610            Adk60610 Angiogene
     c      23    394    8.7   5853  12  ADP73233            Adp73233 Angiogene
     c      24    393    8.7    393  12  ADK60263            Adk60263 Antisense
     c      25    393    8.7    393  12  ADK60564            Adk60564 Antisense
     c      26    393    8.7    393  12  ADP73187            Adp73187 Angiogene
     c      27    363    8.0    482  10  ADD32881            Add32881 Human mit
            28    331    7.3    331   6  AAS61782            Aas61782 Lung smal
            29    259    5.7    518   4  AAI42717            Aai42717 Probe #11
            30    259    5.7    518   4  AAK36916            Aak36916 Human bon
            31    259    5.7    518   4  AAK11093            Aak11093 Human bra
            32    259    5.7    518   4  ABS36587            Abs36587 Human liv
            33    259    5.7    518   6  ABS10924            Abs10924 Human gen
            34    187    4.1    436   3  AAZ58765            Aaz58765 Human hun
            35    184    4.1    184   4  AAI55778            Aai55778 Probe #24
            36    184    4.1    184   4  AAK49859            Aak49859 Human bon
            37    184    4.1    184   4  AAK23763            Aak23763 Human bra
            38    184    4.1    184   4  ABS49496            Abs49496 Human liv
            39    184    4.1    184   6  ABS23356            Abs23356 Human gen
            40    175    3.9    279   3  AAZ58780            Aaz58780 Human hun
            41    163    3.6    404  10  ACC85536            Acc85536 Human HIP
            42    163    3.6    404  14  AEB71169            Aeb71169 DNA of HI
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43      148     3.3     485  3  AAZ58769              Aaz58769 Human hun
44      144     3.2     565  3  AAZ58760              Aaz58760 Human hun
45      143     3.2     577  4  AAI17388              Aai17388 Probe #73
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ALIGNMENTS

RESULT 1
ACC85533
ID   ACC85533 standard; DNA; 4534 BP.
XX
AC   ACC85533;
XX
DT   15-OCT-2003   (first entry)
XX
DE   Human HIP1 cancer marker coding sequence.
XX
KW   Human; HIP1; cancer; cancer marker; epithelial cancer; cytostatic; gene;
KW   ds.
XX
OS   Homo sapiens.
XX
PN   WO2003043566-A2.
XX
PD   30-MAY-2003.
XX
PF   12-NOV-2002; 2002WO-US036175.
XX
PR   15-NOV-2001; 2001US-0335276P.
PR   06-DEC-2001; 2001US-00007047.
XX
PA   (UNMI) UNIV MICHIGAN.
XX
PI   Ross T, Mizukami I, Roa D;
XX
DR   WPI; 2003-457565/43.
XX
PT   New antibody binding to HIP1 but not to normal epithelium, useful for
PT   diagnosing and treating epithelial cancers, particularly colon and
PT   prostate cancer.
XX
PS   Disclosure; Fig 7; 143pp; English.
XX
CC   The present invention relates to an antibody that specifically binds to
CC   HIP1 but does not specifically bind to the normal epithelium of prostate
CC   or colon. The antibody can be used for diagnosing and treating epithelial
CC   cancers, particularly colon and prostate cancer. The present sequence is
CC   the human HIP1 coding sequence
XX
SQ   Sequence 4534 BP; 1176 A; 1230 C; 1232 G; 894 T; 0 U; 2 Other;

   Query Match   100.0%; Score 4534; DB 10; Length 4534;
   Best Local Similarity   100.0%; Pred. No. 0;
   Matches 4534; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 CCAAGCTTGGTACCCCCGGGGCAGCCGAGGGCCCCTGACTCGGCTCCTCGCGGCGACATG 60
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Db      1 CCAAGCTTGGTACCCCCGGGGCAGCCGAGGGCCCCTGACTCGGCTCCTCGCGGCGACATG 60

Qy     61 GATCGGATGGCCAGCTCCATGAAGCAGGTGCCCAACCCACTGCCCAAGGTGCTGAGCCGG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GATCGGATGGCCAGCTCCATGAAGCAGGTGCCCAACCCACTGCCCAAGGTGCTGAGCCGG 120

Qy    121 CGCGGGGTCGGCGCTGGGCTGGAGGCGGCGGAGCGCGAGAGCTTCGAGCGGACTCAGACT 180
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Db    121 CGCGGGGTCGGCGCTGGGCTGGAGGCGGCGGAGCGCGAGAGCTTCGAGCGGACTCAGACT 180

Qy    181 GTCAGCATCAATAAGGCCATTAATACGCAGGAAGTGGCTGTAAAGGAAAAACACGCCAGA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GTCAGCATCAATAAGGCCATTAATACGCAGGAAGTGGCTGTAAAGGAAAAACACGCCAGA 240

Qy    241 ACGTGCATACTGGGCACCCACCATGAGAAAGGGGCACAGACCTTCTGGTCTGTTGTCAAC 300
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Db    241 ACGTGCATACTGGGCACCCACCATGAGAAAGGGGCACAGACCTTCTGGTCTGTTGTCAAC 300

Qy    301 CGCCTGCCTCTGTCTAGCAACGCAGTGCTCTGCTGGAAGTTCTGCCATGTGTTCCACAAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CGCCTGCCTCTGTCTAGCAACGCAGTGCTCTGCTGGAAGTTCTGCCATGTGTTCCACAAA 360

Qy    361 CTCCTCCGAGATGGACACCCGAACGTCCTGAAGGACTCTCTGAGATACAGAAATGAATTG 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CTCCTCCGAGATGGACACCCGAACGTCCTGAAGGACTCTCTGAGATACAGAAATGAATTG 420

Qy    421 AGTGACATGAGCAGGATGTGGGGCTACCTGAGCGAGGGGTATGGCCAGCTGTGCAGCATC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AGTGACATGAGCAGGATGTGGGGCTACCTGAGCGAGGGGTATGGCCAGCTGTGCAGCATC 480

Qy    481 TACCTGAAACTGCTAAGAACCAAGATGGAGTACCACACCAAAAATCCCAGGTTCCCAGGC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 TACCTGAAACTGCTAAGAACCAAGATGGAGTACCACACCAAAAATCCCAGGTTCCCAGGC 540

Qy    541 AACCTGCAGATGAGTGACCGCCAGCTGGACGAGGCTGGAGAAAGTGACGTGAACAACTTT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 AACCTGCAGATGAGTGACCGCCAGCTGGACGAGGCTGGAGAAAGTGACGTGAACAACTTT 600

Qy    601 TCCCAGTTAACAGTGGAGATGTTTGACTACCTGGAGTGTGAACTCAACCTCTTCCAAACA 660
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Db    601 TCCCAGTTAACAGTGGAGATGTTTGACTACCTGGAGTGTGAACTCAACCTCTTCCAAACA 660

Qy    661 GTATTCAACTCCCTGGACATGTCCCGCTCTGTGTCCGTGACGGCAGCAGGGCAGTGCCGC 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GTATTCAACTCCCTGGACATGTCCCGCTCTGTGTCCGTGACGGCAGCAGGGCAGTGCCGC 720

Qy    721 CTCGCCCCGCTGATCCAGGTCATCTTGGACTGCAGCCACCTTTATGACTACACTGTCAAG 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CTCGCCCCGCTGATCCAGGTCATCTTGGACTGCAGCCACCTTTATGACTACACTGTCAAG 780

Qy    781 CTTCTCTTCAAACTCCACTCCTGCCTCCCAGCTGACACCCTGCAAGGCCACCGGGACCGC 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 CTTCTCTTCAAACTCCACTCCTGCCTCCCAGCTGACACCCTGCAAGGCCACCGGGACCGC 840

Qy    841 TTCATGGAGCAGTTTACAAAGTTGAAAGATCTGTTCTACCGCTCCAGCAACCTGCAGTAC 900
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Db     841  TTCATGGAGCAGTTTACAAAGTTGAAAGATCTGTTCTACCGCTCCAGCAACCTGCAGTAC  900

Qy     901  TTCAAGCGGCTCATTCAGATCCCCCAGCTGCCTGAGAACCCACCCAACTTCCTGCGAGCC  960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901  TTCAAGCGGCTCATTCAGATCCCCCAGCTGCCTGAGAACCCACCCAACTTCCTGCGAGCC  960

Qy     961  TCAGCCCTGTCAGAACATATCAGCCCTGTGGTGGTGATCCCTGCAGAGGCCTCATCCCCC  1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961  TCAGCCCTGTCAGAACATATCAGCCCTGTGGTGGTGATCCCTGCAGAGGCCTCATCCCCC  1020

Qy    1021  GACAGCGAGCCAGTCCTAGAGAAGGATGACCTCATGGACATGGATGCCTCTCAGCAGAAT  1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021  GACAGCGAGCCAGTCCTAGAGAAGGATGACCTCATGGACATGGATGCCTCTCAGCAGAAT  1080

Qy    1081  TTATTTGACAACAAGTTTGATGACATCTTTGGCAGTTCATTCAGCAGTGATCCCTTCAAT  1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081  TTATTTGACAACAAGTTTGATGACATCTTTGGCAGTTCATTCAGCAGTGATCCCTTCAAT  1140

Qy    1141  TTCAACAGTCAAAATGGTGTGAACAAGGATGAGAAGGACCACTTAATTGAGCGACTATAC  1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141  TTCAACAGTCAAAATGGTGTGAACAAGGATGAGAAGGACCACTTAATTGAGCGACTATAC  1200

Qy    1201  AGAGAGATCAGTGGATTGAAGGCACAGCTAGAAAACATGAAGACTGAGAGCCAGCGGGTT  1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201  AGAGAGATCAGTGGATTGAAGGCACAGCTAGAAAACATGAAGACTGAGAGCCAGCGGGTT  1260

Qy    1261  GTGCTGCAGCTGAAGGGCCACGTCAGCGAGCTGGAAGCAGATCTGGCCGAGCAGCAGCAC  1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261  GTGCTGCAGCTGAAGGGCCACGTCAGCGAGCTGGAAGCAGATCTGGCCGAGCAGCAGCAC  1320

Qy    1321  CTGCGGCAGCAGGCGGCCGACGACTGTGAATTCCTGCGGGCAGAACTGGACGAGCTCAGG  1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321  CTGCGGCAGCAGGCGGCCGACGACTGTGAATTCCTGCGGGCAGAACTGGACGAGCTCAGG  1380

Qy    1381  AGGCAGCGGGAGGACACCGAGAAGGCTCAGCGGAGCCTGTCTGAGATAGAAAGGAAAGCT  1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381  AGGCAGCGGGAGGACACCGAGAAGGCTCAGCGGAGCCTGTCTGAGATAGAAAGGAAAGCT  1440

Qy    1441  CAAGCCAATGAACAGCGATATAGCAAGCTAAAGGAGAAGTACAGCGAGCTGGTTCAGAAC  1500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441  CAAGCCAATGAACAGCGATATAGCAAGCTAAAGGAGAAGTACAGCGAGCTGGTTCAGAAC  1500

Qy    1501  CACGCTGACCTGCTGCGGAAGAATGCAGAGGTGACCAAACAGGTGTCCATGGCCAGACAA  1560
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501  CACGCTGACCTGCTGCGGAAGAATGCAGAGGTGACCAAACAGGTGTCCATGGCCAGACAA  1560

Qy    1561  GCCCAGGTAGATTTGGAACGAGAGAAAAAGAGCTGGAGGATTCGTTGGAGCGCATCAGT  1620
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561  GCCCAGGTAGATTTGGAACGAGAGAAAAAGAGCTGGAGGATTCGTTGGAGCGCATCAGT  1620

Qy    1621  GACCAGGGCCAGCGGAAGACTCAAGAACAGCTGGAAGTTCTAGAGAGCTTGAAGCAGGAA  1680
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1621  GACCAGGGCCAGCGGAAGACTCAAGAACAGCTGGAAGTTCTAGAGAGCTTGAAGCAGGAA  1680

Qy    1681  CTTGCCACAAGCCAACGGGAGCTTCAGGTTCTGCAAGGCAGCCTGGAAACTTCTGCCCAG  1740
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1681  CTTGCCACAAGCCAACGGGAGCTTCAGGTTCTGCAAGGCAGCCTGGAAACTTCTGCCCAG  1740
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Qy    1741  TCAGAAGCAAACTGGGCAGCCGAGTTCGCCGAGCTAGAGAAGGAGCGGGACAGCCTGGTG  1800
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1741  TCAGAAGCAAACTGGGCAGCCGAGTTCGCCGAGCTAGAGAAGGAGCGGGACAGCCTGGTG  1800

Qy    1801  AGTGGCGCAGCTCATAGGGAGGAGGAATTATCTGCTCTTCGGAAAGAACTGCAGGACACT  1860
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1801  AGTGGCGCAGCTCATAGGGAGGAGGAATTATCTGCTCTTCGGAAAGAACTGCAGGACACT  1860

Qy    1861  CAGCTCAAACTGGCCAGCACAGAGGAATCTATGTGCCAGCTTGCCAAAGACCAACGAAAA  1920
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1861  CAGCTCAAACTGGCCAGCACAGAGGAATCTATGTGCCAGCTTGCCAAAGACCAACGAAAA  1920

Qy    1921  ATGCTTCTGGTGGGGTCCAGGAAGGCTGCGGAGCAGGTGATACAAGACGCCCTGAACCAG  1980
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921  ATGCTTCTGGTGGGGTCCAGGAAGGCTGCGGAGCAGGTGATACAAGACGCCCTGAACCAG  1980

Qy    1981  CTTGAAGAACCTCCTCTCATCAGCTGCGCTGGGTCTGCAGATCACCTCCTCTCCACGGTC  2040
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1981  CTTGAAGAACCTCCTCTCATCAGCTGCGCTGGGTCTGCAGATCACCTCCTCTCCACGGTC  2040

Qy    2041  ACATCCATTTCCAGCTGCATCGAGCAACTGGAGAAAAGCTGGAGCCAGTATCTGGCCTGC  2100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2041  ACATCCATTTCCAGCTGCATCGAGCAACTGGAGAAAAGCTGGAGCCAGTATCTGGCCTGC  2100

Qy    2101  CCAGAAGACATCAGTGGACTTCTCCATTCCATAACCCTGCTGGCCCACTTGACCAGCGAC  2160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2101  CCAGAAGACATCAGTGGACTTCTCCATTCCATAACCCTGCTGGCCCACTTGACCAGCGAC  2160

Qy    2161  GCCATTGCTCATGGTGCCACCACCTGCCTCAGAGCCCCACCTGAGCCTGCCGACTCACTG  2220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2161  GCCATTGCTCATGGTGCCACCACCTGCCTCAGAGCCCCACCTGAGCCTGCCGACTCACTG  2220

Qy    2221  ACCGAGGCCTGTAAGCAGTATGGCAGGGAAACCCTCGCCTACCTGGCCTCCCTGGAGGAA  2280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2221  ACCGAGGCCTGTAAGCAGTATGGCAGGGAAACCCTCGCCTACCTGGCCTCCCTGGAGGAA  2280

Qy    2281  GAGGGAAGCCTTGAGAATGCCGACAGCACAGCCATGAGGAACTGCCTGAGCAAGATCAAG  2340
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2281  GAGGGAAGCCTTGAGAATGCCGACAGCACAGCCATGAGGAACTGCCTGAGCAAGATCAAG  2340

Qy    2341  GCCATCGGCGAGGAGCTCCTGCCCAGGGGACTGGACATCAAGCAGGAGGAGCTGGGGGAC  2400
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2341  GCCATCGGCGAGGAGCTCCTGCCCAGGGGACTGGACATCAAGCAGGAGGAGCTGGGGGAC  2400

Qy    2401  CTGGTGGACAAGGAGATGGCGGCCACTTCAGCTGCTATTGAAACTGCCACGGCCAGAATA  2460
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2401  CTGGTGGACAAGGAGATGGCGGCCACTTCAGCTGCTATTGAAACTGCCACGGCCAGAATA  2460

Qy    2461  GAGGAGATGCTCAGCAAATCCCGAGCAGGAGACACAGGAGTCAAATTGGAGGTGAATGAA  2520
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2461  GAGGAGATGCTCAGCAAATCCCGAGCAGGAGACACAGGAGTCAAATTGGAGGTGAATGAA  2520

Qy    2521  AGGATCCTTGGTTGCTGTACCAGCCTCATGCAAGCTATTCAGGTGCTCATCGTGGCCTCT  2580
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2521  AGGATCCTTGGTTGCTGTACCAGCCTCATGCAAGCTATTCAGGTGCTCATCGTGGCCTCT  2580
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Qy   2581 AAGGACCTCCAGAGAGAGATTGTGGAGAGCGGCAGGGGTACAGCATCCCCTAAAGAGTTT 2640
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2581 AAGGACCTCCAGAGAGAGATTGTGGAGAGCGGCAGGGGTACAGCATCCCCTAAAGAGTTT 2640

Qy   2641 TATGCCAAGAACTCTCGATGGACAGAAGGACTTATCTCAGCCTCCAAGGCTGTGGGCTGG 2700
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 TATGCCAAGAACTCTCGATGGACAGAAGGACTTATCTCAGCCTCCAAGGCTGTGGGCTGG 2700

Qy   2701 GGAGCCACTGTCATGGTGGATGCAGCTGATCTGGTGGTACAAGGCAGAGGGAAATTTGAG 2760
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 GGAGCCACTGTCATGGTGGATGCAGCTGATCTGGTGGTACAAGGCAGAGGGAAATTTGAG 2760

Qy   2761 GAGCTAATGGTGTGTTCTCATGAAATTGCTGCTAGCACAGCCCAGCTTGTGGCTGCATCC 2820
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 GAGCTAATGGTGTGTTCTCATGAAATTGCTGCTAGCACAGCCCAGCTTGTGGCTGCATCC 2820

Qy   2821 AAGGTGAAAGCTGATAAGGACAGCCCCAACCTAGCCCAGCTGCAGCAGGCCTCTCGGGGA 2880
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 AAGGTGAAAGCTGATAAGGACAGCCCCAACCTAGCCCAGCTGCAGCAGGCCTCTCGGGGA 2880

Qy   2881 GTGAACCAGGCCACTGCCGGCGTTGTGGCCTCAACCATTTCCGGCAAATCACAGATCGAA 2940
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GTGAACCAGGCCACTGCCGGCGTTGTGGCCTCAACCATTTCCGGCAAATCACAGATCGAA 2940

Qy   2941 GAGACAGACAACATGGACTTCTCAAGCATGACGCTGACACAGATCAAACGCCAAGAGATG 3000
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 GAGACAGACAACATGGACTTCTCAAGCATGACGCTGACACAGATCAAACGCCAAGAGATG 3000

Qy   3001 GATTCTCAGGTTAGGGTGCTAGAGCTAGAAAATGAATTGCAGAAGGAGCGTCAAAAACTG 3060
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 GATTCTCAGGTTAGGGTGCTAGAGCTAGAAAATGAATTGCAGAAGGAGCGTCAAAAACTG 3060

Qy   3061 GGAGAGCTTCGGAAAAAGCACTACGAGCTTGCTGGTGTTGCTGAGGGCTGGGAAGAAGGA 3120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 GGAGAGCTTCGGAAAAAGCACTACGAGCTTGCTGGTGTTGCTGAGGGCTGGGAAGAAGGA 3120

Qy   3121 ACAGAGGCATCTCCACCTACACTGCAAGAAGTGGTAACCGAAAAAGAATAGAGCCAAACC 3180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 ACAGAGGCATCTCCACCTACACTGCAAGAAGTGGTAACCGAAAAAGAATAGAGCCAAACC 3180

Qy   3181 AACACCCCATATGTCAGTGTAAATCCTTGTTACCTATCTCGTGTGTGTTATTTCCCCAGC 3240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 AACACCCCATATGTCAGTGTAAATCCTTGTTACCTATCTCGTGTGTGTTATTTCCCCAGC 3240

Qy   3241 CACAGGCCAAATCCTTGGAGTCCCAGGGGCAGCCACACCACTGCCATTACCCAGTGCCGA 3300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 CACAGGCCAAATCCTTGGAGTCCCAGGGGCAGCCACACCACTGCCATTACCCAGTGCCGA 3300

Qy   3301 GGACATGCATGACACTTCCAAAGACTCCCTCCATAGCGACACCCTTTCTGTTTGGACCCA 3360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 GGACATGCATGACACTTCCAAAGACTCCCTCCATAGCGACACCCTTTCTGTTTGGACCCA 3360

Qy   3361 TGGATTTCCACTGCTTCTTATGGTGGTTGGTTGGGTTTTTTGGTTTTGTTTTTTTTTTTT 3420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 TGGATTTCCACTGCTTCTTATGGTGGTTGGTTGGGTTTTTTGGTTTTGTTTTTTTTTTTT 3420

Qy   3421 AAGTTTCACTCACATAGCCAACTCTCCCAAAGGGCACACCCCTGGGGCTGAGTCTCCAGG 3480
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        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3421 AAGTTTCACTCACATAGCCAACTCTCCCAAAGGGCACACCCCTGGGGCTGAGTCTCCAGG 3480

Qy  3481 GCCCCCCAACTGTGGTAGCTCCAGCGATGGTGCTGCCCAGGCCTCTCGGTGCTCCATCTC 3540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3481 GCCCCCCAACTGTGGTAGCTCCAGCGATGGTGCTGCCCAGGCCTCTCGGTGCTCCATCTC 3540

Qy  3541 CGCCTCCACACTGACCAAGTGCTGGCCCACCCAGTCCATGCTCCAGGGTCAGGCGGAGCT 3600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3541 CGCCTCCACACTGACCAAGTGCTGGCCCACCCAGTCCATGCTCCAGGGTCAGGCGGAGCT 3600

Qy  3601 GCTGAGTGACAGCTTTCCTCAAAAAGCAGAAGGAGAGTGAGTGCCTTTCCTCCTAAAGC 3660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3601 GCTGAGTGACAGCTTTCCTCAAAAAGCAGAAGGAGAGTGAGTGCCTTTCCTCCTAAAGC 3660

Qy  3661 TGAATCCCGGCGGAAAGCCTCTGTCCGCCTTTACAAGGGAGAAGACAACAGAAAGAGGGA 3720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3661 TGAATCCCGGCGGAAAGCCTCTGTCCGCCTTTACAAGGGAGAAGACAACAGAAAGAGGGA 3720

Qy  3721 CAAGAGGGTTCACACAGCCCAGTTCCCGTGACGAGGCTCAAAAACTTGATCACATGCTTG 3780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3721 CAAGAGGGTTCACACAGCCCAGTTCCCGTGACGAGGCTCAAAAACTTGATCACATGCTTG 3780

Qy  3781 AATGGAGCTGGTGAGATCAACAACACTACTTCCCTGCCGGAATGAACTGTCCGTGAATGG 3840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3781 AATGGAGCTGGTGAGATCAACAACACTACTTCCCTGCCGGAATGAACTGTCCGTGAATGG 3840

Qy  3841 TCTCTGTCAAGCGGGCCGTCTCCCTTGGCCCAGAGACGGAGTGTGGGAGTGATTCCCAAC 3900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3841 TCTCTGTCAAGCGGGCCGTCTCCCTTGGCCCAGAGACGGAGTGTGGGAGTGATTCCCAAC 3900

Qy  3901 TCCTTTCTGCAGACGTCTGCCTTGGCATCCTCTTGAATAGGAAGATCGTTCCACCTTCTA 3960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3901 TCCTTTCTGCAGACGTCTGCCTTGGCATCCTCTTGAATAGGAAGATCGTTCCACCTTCTA 3960

Qy  3961 CGCAATTGACAAACCCGGAAGATCAGATGCAATTGCTCCCATCAGGGAAGAACCCTATAC 4020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  3961 CGCAATTGACAAACCCGGAAGATCAGATGCAATTGCTCCCATCAGGGAAGAACCCTATAC 4020

Qy  4021 TTGGTTTGCTACCCTTAGTATTTATTACTAACCTCCCTTAAGCAGCAACAGCCTACAAAG 4080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4021 TTGGTTTGCTACCCTTAGTATTTATTACTAACCTCCCTTAAGCAGCAACAGCCTACAAAG 4080

Qy  4081 AGATGCTTGGAGCAATCAGAACTTCAGGTGTGACTCTAGCAAAGCTCATCTTTCTGCCCG 4140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4081 AGATGCTTGGAGCAATCAGAACTTCAGGTGTGACTCTAGCAAAGCTCATCTTTCTGCCCG 4140

Qy  4141 GCTACATCAGCCTTCAAGAATCAGAAGAAAGGCCAAGGTGCTGGACTGTTACTGACTTGG 4200
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4141 GCTACATCAGCCTTCAAGAATCAGAAGAAAGGCCAAGGTGCTGGACTGTTACTGACTTGG 4200

Qy  4201 ATCCCAAAGCAAGGAGATCATTTGGAGCTCTTGGGTCAGAGAAAATGAGAAAGGACAGAG 4260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  4201 ATCCCAAAGCAAGGAGATCATTTGGAGCTCTTGGGTCAGAGAAAATGAGAAAGGACAGAG 4260

Qy  4261 CCAGCGGCTCCAACTCCTTTCAGCCACATGCCCCAGGCTCTCGCTGCCCTGTGGACAGGA 4320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        4261  CCAGCGGCTCCAACTCCTTTCAGCCACATGCCCCAGGCTCTCGCTGCCCTGTGGACAGGA 4320

Qy        4321  TGAGGACAGAGGGCACATGAACAGCTTGCCAGGGATGGGCAGCCCAACAGCACTTTTCCT 4380
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4321  TGAGGACAGAGGGCACATGAACAGCTTGCCAGGGATGGGCAGCCCAACAGCACTTTTCCT 4380

Qy        4381  CTTCTAGATGGACCCCAGCATTTAAGTGACCTTCTGATCTTGGGAAAACAGCGTCTTCCT 4440
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4381  CTTCTAGATGGACCCCAGCATTTAAGTGACCTTCTGATCTTGGGAAAACAGCGTCTTCCT 4440

Qy        4441  TCTTTATCTATAGCAACTCATTGGTGGTAGCCATCAAGCACTTCGGAATTCCTGCAGCCC 4500
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4441  TCTTTATCTATAGCAACTCATTGGTGGTAGCCATCAAGCACTTCGGAATTCCTGCAGCCC 4500

Qy        4501  GGGCGGCCGCTCGAGCATGCNNTAGAGGGCCCTA 4534
                ||||||||||||||||||||||||||||||||||
Db        4501  GGGCGGCCGCTCGAGCATGCNNTAGAGGGCCCTA 4534
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RESULT 2
AEB71165
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ID    AEB71165 standard; DNA; 4534 BP.
XX
AC    AEB71165;
XX
DT    20-OCT-2005   (first entry)
XX
DE    DNA encoding full length HIP1, SEQ ID NO:1.
XX
KW    Cancer; cytosatic; diagnosis; genetic marker; HIP1; immunodiagnosis;
KW    drug screening; western blot; ELISA; ds; gene.
XX
OS    Homo sapiens.
XX
FH    Key             Location/Qualifiers
FT    CDS             58. .3171
FT                    /*tag=  a
FT                    /product= "HIP1"
XX
PN    WO2005072457-A2.
XX
PD    11-AUG-2005.
XX
PF    28-JAN-2005; 2005WO-US003330.
XX
PR    29-JAN-2004; 2004US-00767325.
XX
PA    (UNMI ) UNIV MICHIGAN.
XX
PI    Ross TS,  Mizukami IF;
XX
DR    WPI; 2005-582467/59.
DR    P-PSDB; AEB71166.
XX
PT    Detecting cancer (especially prostate or colon cancer) comprises
PT    providing a sample from a subject suspected of having cancer, and
PT    detecting the presence or absence of antibodies to HIP1 in the sample.
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     Query Match                100.0%;   Score 4534;   DB 14;   Length 4534;
     Best Local Similarity      100.0%;   Pred. No. 0;
     Matches 4534;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;


Qy         1 CCAAGCTTGGTACCCCCGGGGCAGCCGAGGGCCCCTGACTCGGCTCCTCGCGGCGACATG 60
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 CCAAGCTTGGTACCCCCGGGGCAGCCGAGGGCCCCTGACTCGGCTCCTCGCGGCGACATG 60


Qy        61 GATCGGATGGCCAGCTCCATGAAGCAGGTGCCCAACCCACTGCCCAAGGTGCTGAGCCGG 120
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 GATCGGATGGCCAGCTCCATGAAGCAGGTGCCCAACCCACTGCCCAAGGTGCTGAGCCGG 120


Qy       121 CGCGGGGTCGGCGCTGGGCTGGAGGCGGCGGAGCGCGAGAGCTTCGAGCGGACTCAGACT 180
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 CGCGGGGTCGGCGCTGGGCTGGAGGCGGCGGAGCGCGAGAGCTTCGAGCGGACTCAGACT 180


Qy       181 GTCAGCATCAATAAGGCCATTAATACGCAGGAAGTGGCTGTAAAGGAAAAACACGCCAGA 240
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 GTCAGCATCAATAAGGCCATTAATACGCAGGAAGTGGCTGTAAAGGAAAAACACGCCAGA 240


Qy       241 ACGTGCATACTGGGCACCCACCATGAGAAAGGGGCACAGACCTTCTGGTCTGTTGTCAAC 300
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 ACGTGCATACTGGGCACCCACCATGAGAAAGGGGCACAGACCTTCTGGTCTGTTGTCAAC 300


Qy       301 CGCCTGCCTCTGTCTAGCAACGCAGTGCTCTGCTGGAAGTTCTGCCATGTGTTCCACAAA 360
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 CGCCTGCCTCTGTCTAGCAACGCAGTGCTCTGCTGGAAGTTCTGCCATGTGTTCCACAAA 360


Qy       361 CTCCTCCGAGATGGACACCCGAACGTCCTGAAGGACTCTCTGAGATACAGAAATGAATTG 420
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 CTCCTCCGAGATGGACACCCGAACGTCCTGAAGGACTCTCTGAGATACAGAAATGAATTG 420


Qy       421 AGTGACATGAGCAGGATGTGGGGCTACCTGAGCGAGGGGTATGGCCAGCTGTGCAGCATC 480
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 AGTGACATGAGCAGGATGTGGGGCTACCTGAGCGAGGGGTATGGCCAGCTGTGCAGCATC 480
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Qy    481  TACCTGAAACTGCTAAGAACCAAGATGGAGTACCACACCAAAAATCCCAGGTTCCCAGGC  540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  TACCTGAAACTGCTAAGAACCAAGATGGAGTACCACACCAAAAATCCCAGGTTCCCAGGC  540

Qy    541  AACCTGCAGATGAGTGACCGCCAGCTGGACGAGGCTGGAGAAAGTGACGTGAACAACTTT  600
           . |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  AACCTGCAGATGAGTGACCGCCAGCTGGACGAGGCTGGAGAAAGTGACGTGAACAACTTT  600

Qy    601  TCCCAGTTAACAGTGGAGATGTTTGACTACCTGGAGTGTGAACTCAACCTCTTCCAAACA  660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  TCCCAGTTAACAGTGGAGATGTTTGACTACCTGGAGTGTGAACTCAACCTCTTCCAAACA  660

Qy    661  GTATTCAACTCCCTGGACATGTCCCGCTCTGTGTCCGTGACGGCAGCAGGGCAGTGCCGC  720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661  GTATTCAACTCCCTGGACATGTCCCGCTCTGTGTCCGTGACGGCAGCAGGGCAGTGCCGC  720

Qy    721  CTCGCCCCGCTGATCCAGGTCATCTTGGACTGCAGCCACCTTTATGACTACACTGTCAAG  780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  CTCGCCCCGCTGATCCAGGTCATCTTGGACTGCAGCCACCTTTATGACTACACTGTCAAG  780

Qy    781  CTTCTCTTCAAACTCCACTCCTGCCTCCCAGCTGACACCCTGCAAGGCCACCGGGACCGC  840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  CTTCTCTTCAAACTCCACTCCTGCCTCCCAGCTGACACCCTGCAAGGCCACCGGGACCGC  840

Qy    841  TTCATGGAGCAGTTTACAAAGTTGAAAGATCTGTTCTACCGCTCCAGCAACCTGCAGTAC  900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  TTCATGGAGCAGTTTACAAAGTTGAAAGATCTGTTCTACCGCTCCAGCAACCTGCAGTAC  900

Qy    901  TTCAAGCGGCTCATTCAGATCCCCCAGCTGCCTGAGAACCCACCCAACTTCCTGCGAGCC  960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901  TTCAAGCGGCTCATTCAGATCCCCCAGCTGCCTGAGAACCCACCCAACTTCCTGCGAGCC  960

Qy    961  TCAGCCCTGTCAGAACATATCAGCCCTGTGGTGGTGATCCCTGCAGAGGCCTCATCCCCC  1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  TCAGCCCTGTCAGAACATATCAGCCCTGTGGTGGTGATCCCTGCAGAGGCCTCATCCCCC  1020

Qy   1021  GACAGCGAGCCAGTCCTAGAGAAGGATGACCTCATGGACATGGATGCCTCTCAGCAGAAT  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  GACAGCGAGCCAGTCCTAGAGAAGGATGACCTCATGGACATGGATGCCTCTCAGCAGAAT  1080

Qy   1081  TTATTTGACAACAAGTTTGATGACATCTTTGGCAGTTCATTCAGCAGTGATCCCTTCAAT  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  TTATTTGACAACAAGTTTGATGACATCTTTGGCAGTTCATTCAGCAGTGATCCCTTCAAT  1140

Qy   1141  TTCAACAGTCAAAATGGTGTGAACAAGGATGAGAAGGACCACTTAATTGAGCGACTATAC  1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  TTCAACAGTCAAAATGGTGTGAACAAGGATGAGAAGGACCACTTAATTGAGCGACTATAC  1200

Qy   1201  AGAGAGATCAGTGGATTGAAGGCACAGCTAGAAAACATGAAGACTGAGAGCCAGCGGGTT  1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  AGAGAGATCAGTGGATTGAAGGCACAGCTAGAAAACATGAAGACTGAGAGCCAGCGGGTT  1260

Qy   1261  GTGCTGCAGCTGAAGGGCCACGTCAGCGAGCTGGAAGCAGATCTGGCCGAGCAGCAGCAC  1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261  GTGCTGCAGCTGAAGGGCCACGTCAGCGAGCTGGAAGCAGATCTGGCCGAGCAGCAGCAC  1320

Qy   1321  CTGCGGCAGCAGGCGGCCGACGACTGTGAATTCCTGCGGGCAGAACTGGACGAGCTCAGG  1380
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Db   1321   CTGCGGCAGCAGGCGGCCGACGACTGTGAATTCCTGCGGGCAGAACTGGACGAGCTCAGG   1380

Qy   1381   AGGCAGCGGGAGGACACCGAGAAGGCTCAGCGGAGCCTGTCTGAGATAGAAAGGAAAGCT   1440
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Db   1381   AGGCAGCGGGAGGACACCGAGAAGGCTCAGCGGAGCCTGTCTGAGATAGAAAGGAAAGCT   1440

Qy   1441   CAAGCCAATGAACAGCGATATAGCAAGCTAAAGGAGAAGTACAGCGAGCTGGTTCAGAAC   1500
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Db   1441   CAAGCCAATGAACAGCGATATAGCAAGCTAAAGGAGAAGTACAGCGAGCTGGTTCAGAAC   1500

Qy   1501   CACGCTGACCTGCTGCGGAAGAATGCAGAGGTGACCAAACAGGTGTCCATGGCCAGACAA   1560
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Qy   1561   GCCCAGGTAGATTTGGAACGAGAGAAAAAAGAGCTGGAGGATTCGTTGGAGCGCATCAGT   1620
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Db   1561   GCCCAGGTAGATTTGGAACGAGAGAAAAAAGAGCTGGAGGATTCGTTGGAGCGCATCAGT   1620

Qy   1621   GACCAGGGCCAGCGGAAGACTCAAGAACAGCTGGAAGTTCTAGAGAGCTTGAAGCAGGAA   1680
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Db   1621   GACCAGGGCCAGCGGAAGACTCAAGAACAGCTGGAAGTTCTAGAGAGCTTGAAGCAGGAA   1680

Qy   1681   CTTGCCACAAGCCAACGGGAGCTTCAGGTTCTGCAAGGCAGCCTGGAAACTTCTGCCCAG   1740
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Qy   1741   TCAGAAGCAAACTGGGCAGCCGAGTTCGCCGAGCTAGAGAAGGAGCGGGACAGCCTGGTG   1800
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Db   1741   TCAGAAGCAAACTGGGCAGCCGAGTTCGCCGAGCTAGAGAAGGAGCGGGACAGCCTGGTG   1800

Qy   1801   AGTGGCGCAGCTCATAGGGAGGAGGAATTATCTGCTCTTCGGAAAGAACTGCAGGACACT   1860
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Db   1801   AGTGGCGCAGCTCATAGGGAGGAGGAATTATCTGCTCTTCGGAAAGAACTGCAGGACACT   1860

Qy   1861   CAGCTCAAACTGGCCAGCACAGAGGAATCTATGTGCCAGCTTGCCAAAGACCAACGAAAA   1920
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Db   1861   CAGCTCAAACTGGCCAGCACAGAGGAATCTATGTGCCAGCTTGCCAAAGACCAACGAAAA   1920

Qy   1921   ATGCTTCTGGTGGGGTCCAGGAAGGCTGCGGAGCAGGTGATACAAGACGCCCTGAACCAG   1980
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   1921   ATGCTTCTGGTGGGGTCCAGGAAGGCTGCGGAGCAGGTGATACAAGACGCCCTGAACCAG   1980

Qy   1981   CTTGAAGAACCTCCTCTCATCAGCTGCGCTGGGTCTGCAGATCACCTCCTCTCCACGGTC   2040
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Db   1981   CTTGAAGAACCTCCTCTCATCAGCTGCGCTGGGTCTGCAGATCACCTCCTCTCCACGGTC   2040

Qy   2041   ACATCCATTTCCAGCTGCATCGAGCAACTGGAGAAAAGCTGGAGCCAGTATCTGGCCTGC   2100
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Db   2041   ACATCCATTTCCAGCTGCATCGAGCAACTGGAGAAAAGCTGGAGCCAGTATCTGGCCTGC   2100

Qy   2101   CCAGAAGACATCAGTGGACTTCTCCATTCCATAACCCTGCTGGCCCACTTGACCAGCGAC   2160
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   2101   CCAGAAGACATCAGTGGACTTCTCCATTCCATAACCCTGCTGGCCCACTTGACCAGCGAC   2160

Qy   2161   GCCATTGCTCATGGTGCCACCACCTGCCTCAGAGCCCCACCTGAGCCTGCCGACTCACTG   2220
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Db    2161 GCCATTGCTCATGGTGCCACCACCTGCCTCAGAGCCCCACCTGAGCCTGCCGACTCACTG 2220

Qy    2221 ACCGAGGCCTGTAAGCAGTATGGCAGGGAAACCCTCGCCTACCTGGCCTCCCTGGAGGAA 2280
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Db    2221 ACCGAGGCCTGTAAGCAGTATGGCAGGGAAACCCTCGCCTACCTGGCCTCCCTGGAGGAA 2280

Qy    2281 GAGGGAAGCCTTGAGAATGCCGACAGCACAGCCATGAGGAACTGCCTGAGCAAGATCAAG 2340
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Db    2281 GAGGGAAGCCTTGAGAATGCCGACAGCACAGCCATGAGGAACTGCCTGAGCAAGATCAAG 2340

Qy    2341 GCCATCGGCGAGGAGCTCCTGCCCAGGGGACTGGACATCAAGCAGGAGGAGCTGGGGGAC 2400
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Qy    2401 CTGGTGGACAAGGAGATGGCGGCCACTTCAGCTGCTATTGAAACTGCCACGGCCAGAATA 2460
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Db    2401 CTGGTGGACAAGGAGATGGCGGCCACTTCAGCTGCTATTGAAACTGCCACGGCCAGAATA 2460

Qy    2461 GAGGAGATGCTCAGCAAATCCCGAGCAGGAGACACAGGAGTCAAATTGGAGGTGAATGAA 2520
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Db    2461 GAGGAGATGCTCAGCAAATCCCGAGCAGGAGACACAGGAGTCAAATTGGAGGTGAATGAA 2520

Qy    2521 AGGATCCTTGGTTGCTGTACCAGCCTCATGCAAGCTATTCAGGTGCTCATCGTGGCCTCT 2580
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Qy    2581 AAGGACCTCCAGAGAGAGATTGTGGAGAGCGGCAGGGGTACAGCATCCCCTAAAGAGTTT 2640
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Db    2581 AAGGACCTCCAGAGAGAGATTGTGGAGAGCGGCAGGGGTACAGCATCCCCTAAAGAGTTT 2640

Qy    2641 TATGCCAAGAACTCTCGATGGACAGAAGGACTTATCTCAGCCTCCAAGGCTGTGGGCTGG 2700
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Qy    2701 GGAGCCACTGTCATGGTGGATGCAGCTGATCTGGTGGTACAAGGCAGAGGGAAATTTGAG 2760
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Db    2701 GGAGCCACTGTCATGGTGGATGCAGCTGATCTGGTGGTACAAGGCAGAGGGAAATTTGAG 2760

Qy    2761 GAGCTAATGGTGTGTTCTCATGAAATTGCTGCTAGCACAGCCCAGCTTGTGGCTGCATCC 2820
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Qy    2821 AAGGTGAAAGCTGATAAGGACAGCCCCAACCTAGCCCAGCTGCAGCAGGCCTCTCGGGGA 2880
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Db    2821 AAGGTGAAAGCTGATAAGGACAGCCCCAACCTAGCCCAGCTGCAGCAGGCCTCTCGGGGA 2880

Qy    2881 GTGAACCAGGCCACTGCCGGCGTTGTGGCCTCAACCATTTCCGGCAAATCACAGATCGAA 2940
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Qy    2941 GAGACAGACAACATGGACTTCTCAAGCATGACGCTGACACAGATCAAACGCCAAGAGATG 3000
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Db    2941 GAGACAGACAACATGGACTTCTCAAGCATGACGCTGACACAGATCAAACGCCAAGAGATG 3000

Qy    3001 GATTCTCAGGTTAGGGTGCTAGAGCTAGAAAATGAATTGCAGAAGGAGCGTCAAAAACTG 3060
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Db    3001 GATTCTCAGGTTAGGGTGCTAGAGCTAGAAAATGAATTGCAGAAGGAGCGTCAAAAACTG 3060
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Qy    3061 GGAGAGCTTCGGAAAAAGCACTACGAGCTTGCTGGTGTTGCTGAGGGCTGGGAAGAAGGA 3120
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Db    3061 GGAGAGCTTCGGAAAAAGCACTACGAGCTTGCTGGTGTTGCTGAGGGCTGGGAAGAAGGA 3120

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Qy    3181 AACACCCCATATGTCAGTGTAAATCCTTGTTACCTATCTCGTGTGTGTTATTTCCCCAGC 3240
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Qy    3241 CACAGGCCAAATCCTTGGAGTCCCAGGGGCAGCCACACCACTGCCATTACCCAGTGCCGA 3300
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Qy    3841 TCTCTGTCAAGCGGGCCGTCTCCCTTGGCCCAGAGACGGAGTGTGGGAGTGATTCCCAAC 3900
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Db    3841 TCTCTGTCAAGCGGGCCGTCTCCCTTGGCCCAGAGACGGAGTGTGGGAGTGATTCCCAAC 3900
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Qy    3901 TCCTTTCTGCAGACGTCTGCCTTGGCATCCTCTTGAATAGGAAGATCGTTCCACCTTCTA 3960
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                                 SUMMARIES
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        6    187    4.1     436  3   US-09-085-199B-28         Sequence 28, Appl
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        8    175    3.9     279  3   US-09-085-199B-43         Sequence 43, Appl
        9    148    3.3     485  3   US-09-085-199B-32         Sequence 32, Appl
       10    144    3.2     565  3   US-09-085-199B-23         Sequence 23, Appl
       11    143    3.2     578  3   US-09-085-199B-25         Sequence 25, Appl
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       13    136    3.0     468  3   US-09-085-199B-33         Sequence 33, Appl
       14    126    2.8     418  3   US-09-085-199B-42         Sequence 42, Appl
       15    119    2.6     359  3   US-09-085-199B-30         Sequence 30, Appl
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       22     108    2.4    351   3   US-09-085-199B-41        Sequence 41, Appl
       23     104    2.3    209   3   US-09-085-199B-31        Sequence 31, Appl
       24     103    2.3    437   3   US-09-085-199B-40        Sequence 40, Appl
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ALIGNMENTS

RESULT 1
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; Sequence 4586, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;   APPLICANT: VENTER, J. Craig et al.
;   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;   TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
THEREOF
;   FILE REFERENCE: CL001307
;   CURRENT APPLICATION NUMBER: US/09/949,016
;   CURRENT FILING DATE: 2000-04-14
;   PRIOR APPLICATION NUMBER: 60/241,755
;   PRIOR FILING DATE: 2000-10-20
;   PRIOR APPLICATION NUMBER: 60/237,768
;   PRIOR FILING DATE: 2000-10-03
;   PRIOR APPLICATION NUMBER: 60/231,498
;   PRIOR FILING DATE: 2000-09-08
;   NUMBER OF SEQ ID NOS: 207012
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4586
;   LENGTH: 6628
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-4586

   Query Match   61.3%; Score 2779; DB 3; Length 6628;
   Best Local Similarity   99.8%; Pred. No. 0;

Matches 3179;   Conservative   0;   Mismatches   2;   Indels   4;   Gaps   1;

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OM nucleic - nucleic search, using sw model

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Perfect score:    4534
Sequence:         1 ccaagcttggtaccccccggg..........gcatgcnntagagggcccta 4534


Scoring table:    OLIGO_NUC
                  Gapop 60.0 , Gapext 60.0


Searched:         9793542 seqs, 4134689005 residues


Word size :       0


Total number of hits satisfying chosen parameters:      19587084


Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries


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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.


                              SUMMARIES
                    %
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          2   4534  100.0  4534   8  US-10-767-325-1           Sequence 1, Appli
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          7   3035   66.9  6626   9  US-10-934-998-38          Sequence 38, Appl
          8    973   21.5 65454   7  US-10-293-864-11          Sequence 11, Appl
          9    554   12.2   601   3  US-09-833-790-343         Sequence 343, App
   c     10    394    8.7  5853   9  US-10-934-998-185         Sequence 185, App
   c     11    393    8.7   393   9  US-10-934-998-139         Sequence 139, App
         12    331    7.3   331   3  US-09-833-790-333         Sequence 333, App
         13    259    5.7   518   3  US-09-864-761-13307       Sequence 13307, A
         14    184    4.1   184   3  US-09-864-761-29870       Sequence 29870, A
         15    163    3.6   404   6  US-10-007-047-6           Sequence 6, Appli
         16    163    3.6   404   8  US-10-767-325-6           Sequence 6, Appli
         17    143    3.2   577   3  US-09-864-761-8117        Sequence 8117, Ap
         18    141    3.1   141   3  US-09-864-761-24860       Sequence 24860, A
         19    141    3.1  2080   6  US-10-108-260A-387        Sequence 387, App
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c  20     126     2.8      161    6   US-10-029-386-16651      Sequence 16651, A
c  21     126     2.8      564    6   US-10-029-386-2951       Sequence 2951, Ap
   22      90     2.0     1752    9   US-10-450-763-4807       Sequence 4807, Ap
   23      87     1.9      565    4   US-09-925-065A-518628    Sequence 518628,
   24      76     1.7      219    7   US-10-293-864-13         Sequence 13, Appl
   25      68     1.5      516    7   US-10-293-864-12         Sequence 12, Appl
   26      62     1.4      606    4   US-09-925-065A-600703    Sequence 600703,
   27      60     1.3       60    3   US-09-908-975-13034      Sequence 13034, A
   28      53     1.2      437    4   US-09-925-065A-518627    Sequence 518627,
c  29      32     0.7      141    5   US-10-066-543-969        Sequence 969, App
c  30      31     0.7      962    3   US-09-764-886-40         Sequence 40, Appl
c  31      31     0.7      962    3   US-09-764-891-2651       Sequence 2651, Ap
c  32      31     0.7      962    3   US-09-764-886-40         Sequence 40, Appl
   33      29     0.6      484    3   US-09-918-995-27762      Sequence 27762, A
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   36      29     0.6     3876    3   US-09-849-602-4          Sequence 4, Appli
   37      29     0.6     4457    8   US-10-775-169-259        Sequence 259, App
   38      27     0.6      608    5   US-10-027-632-138843     Sequence 138843,
   39      27     0.6      608    6   US-10-027-632-138843     Sequence 138843,
   40      26     0.6      502    7   US-10-424-599-1463       Sequence 1463, Ap
   41      26     0.6      603    4   US-09-925-065A-911834    Sequence 911834,
c  42      26     0.6      656    4   US-09-925-065A-37147     Sequence 37147, A
c  43      26     0.6      732    4   US-09-925-065A-92008     Sequence 92008, A
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   45      25     0.6       25    7   US-10-719-956-512062     Sequence 512062,
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ALIGNMENTS

RESULT 1
US-10-007-047-1
; Sequence 1, Application US/10007047
; Publication No. US20030124533A1
; GENERAL INFORMATION:
;   APPLICANT: Mizukami, Ikuko
;   APPLICANT: Ross, Theodora
;   APPLICANT: Rao, Dinesh
;   TITLE OF INVENTION: HIP1 Cancer Markers
;   FILE REFERENCE: UM-06692
;   CURRENT APPLICATION NUMBER: US/10/007,047
;   CURRENT FILING DATE: 2001-12-06
;   NUMBER OF SEQ ID NOS: 6
;   SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 4534
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (4521)..(4521)
;   OTHER INFORMATION: The nucleotide "n" can be either a,t,c, or g
;   NAME/KEY: misc_feature
;   LOCATION: (4522)..(4522)
;   OTHER INFORMATION: The nucleotide "n" can be either a,t,c, or g
US-10-007-047-1

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Query Match              100.0%;  Score 4534;  DB 6;   Length 4534;
Best Local Similarity    100.0%;  Pred. No. 0;
Matches 4534;  Conservative     0;  Mismatches     0;  Indels     0;  Gaps     0;

Qy          1 CCAAGCTTGGTACCCCCGGGGCAGCCGAGGGCCCCTGACTCGGCTCCTCGCGGCGACATG 60
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Qy    1681    CTTGCCACAAGCCAACGGGAGCTTCAGGTTCTGCAAGGCAGCCTGGAAACTTCTGCCCAG    1740
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Qy    1981    CTTGAAGAACCTCCTCTCATCAGCTGCGCTGGGTCTGCAGATCACCTCCTCTCCACGGTC    2040
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                        GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:           January 10, 2006, 12:26:01 ; Search time 390 Seconds
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Minimum DB seq length: 0
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	3245	71.6	7239	6	US-10-955-054A-21	Sequence 21, Appl
	2	30	0.7	3391	6	US-10-750-185-64852	Sequence 64852, A
	3	30	0.7	3391	6	US-10-750-623-64852	Sequence 64852, A
	4	29	0.6	4457	6	US-10-775-169-259	Sequence 259, App
	5	25	0.6	25	7	US-11-121-849-111397	Sequence 111397,
	6	25	0.6	25	7	US-11-121-849-111398	Sequence 111398,
	7	25	0.6	25	7	US-11-121-849-111399	Sequence 111399,
	8	25	0.6	25	7	US-11-121-849-111400	Sequence 111400,
	9	25	0.6	25	7	US-11-121-849-111401	Sequence 111401,
	10	25	0.6	25	7	US-11-121-849-111402	Sequence 111402,
	11	25	0.6	25	7	US-11-121-849-111403	Sequence 111403,
	12	25	0.6	25	7	US-11-121-849-111404	Sequence 111404,
	13	25	0.6	25	7	US-11-121-849-111405	Sequence 111405,
	14	25	0.6	25	7	US-11-121-849-111406	Sequence 111406,
	15	24	0.5	1614	6	US-10-750-185-61247	Sequence 61247, A
	16	24	0.5	1614	6	US-10-750-623-61247	Sequence 61247, A
	17	23	0.5	1836	6	US-10-750-185-57119	Sequence 57119, A
	18	23	0.5	1836	6	US-10-750-623-57119	Sequence 57119, A
	19	23	0.5	5152	6	US-10-240-708-74	Sequence 74, Appl
c	20	23	0.5	187745	7	US-11-121-086-83	Sequence 83, Appl
	21	22	0.5	25	7	US-11-121-849-111396	Sequence 111396,
	22	22	0.5	201	6	US-10-995-561-63599	Sequence 63599, A
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RESULT 1
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; Publication No. US20050266420A1
; GENERAL INFORMATION:
;  APPLICANT: PUSZTAI, LAJOS
;  APPLICANT:  SYMMANS, W. FRASER
;  APPLICANT:  HESS, KENNETH R.
;  APPLICANT:  AYERS, MARK
;  APPLICANT:  STEC, JAMES
;  TITLE OF INVENTION: MULTIGENE PREDICTORS OF RESPONSE TO CHEMOTHERAPY
;  FILE REFERENCE: UTXC:880US
;  CURRENT APPLICATION NUMBER: US/10/955,054A
;  CURRENT FILING DATE:  2004-09-30
;  NUMBER OF SEQ ID NOS: 195
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
;   LENGTH: 7239
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-955-054A-21

    Query Match             71.6%;  Score 3245;  DB 6;  Length 7239;
    Best Local Similarity   99.9%;  Pred. No. 0;
    Matches 3345;  Conservative   0;  Mismatches   2;  Indels   0;  Gaps   0;

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Qy     1937  CCAGGAAGGCTGCGGAGCAGGTGATACAAGACGCCCTGAACCAGCTTGAAGAACCTCCTC  1996
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Qy   2057 GCATCGAGCAACTGGAGAAAAGCTGGAGCCAGTATCTGGCCTGCCCAGAAGACATCAGTG 2116
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Db   2041 GCATCGAGCAACTGGAGAAAAGCTGGAGCCAGTATCTGGCCTGCCCAGAAGACATCAGTG 2100

Qy   2117 GACTTCTCCATTCCATAACCCTGCTGGCCCACTTGACCAGCGACGCCATTGCTCATGGTG 2176
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 GACTTCTCCATTCCATAACCCTGCTGGCCCACTTGACCAGCGACGCCATTGCTCATGGTG 2160

Qy   2177 CCACCACCTGCCTCAGAGCCCCACCTGAGCCTGCCGACTCACTGACCGAGGCCTGTAAGC 2236
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 CCACCACCTGCCTCAGAGCCCCACCTGAGCCTGCCGACTCACTGACCGAGGCCTGTAAGC 2220

Qy   2237 AGTATGGCAGGGAAACCCTCGCCTACCTGGCCTCCCTGGAGGAAGAGGGAAGCCTTGAGA 2296
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 AGTATGGCAGGGAAACCCTCGCCTACCTGGCCTCCCTGGAGGAAGAGGGAAGCCTTGAGA 2280

Qy   2297 ATGCCGACAGCACAGCCATGAGGAACTGCCTGAGCAAGATCAAGGCCATCGGCGAGGAGC 2356
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Db   2281 ATGCCGACAGCACAGCCATGAGGAACTGCCTGAGCAAGATCAAGGCCATCGGCGAGGAGC 2340

Qy   2357 TCCTGCCCAGGGGACTGGACATCAAGCAGGAGGAGCTGGGGGACCTGGTGGACAAGGAGA 2416
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 TCCTGCCCAGGGGACTGGACATCAAGCAGGAGGAGCTGGGGGACCTGGTGGACAAGGAGA 2400

Qy   2417 TGGCGGCCACTTCAGCTGCTATTGAAACTGCCACGGCCAGAATAGAGGAGATGCTCAGCA 2476
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 TGGCGGCCACTTCAGCTGCTATTGAAACTGCCACGGCCAGAATAGAGGAGATGCTCAGCA 2460

Qy   2477 AATCCCGAGCAGGAGACACAGGAGTCAAATTGGAGGTGAATGAAAGGATCCTTGGTTGCT 2536
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2461 AATCCCGAGCAGGAGACACAGGAGTCAAATTGGAGGTGAATGAAAGGATCCTTGGTTGCT 2520

Qy   2537 GTACCAGCCTCATGCAAGCTATTCAGGTGCTCATCGTGGCCTCTAAGGACCTCCAGAGAG 2596
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Db   2521 GTACCAGCCTCATGCAAGCTATTCAGGTGCTCATCGTGGCCTCTAAGGACCTCCAGAGAG 2580

Qy   2597 AGATTGTGGAGAGCGGCAGGGGTACAGCATCCCCTAAAGAGTTTTATGCCAAGAACTCTC 2656
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Db   2581 AGATTGTGGAGAGCGGCAGGGGTACAGCATCCCCTAAAGAGTTTTATGCCAAGAACTCTC 2640

Qy   2657 GATGGACAGAAGGACTTATCTCAGCCTCCAAGGCTGTGGGCTGGGGAGCCACTGTCATGG 2716
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Qy   2717 TGGATGCAGCTGATCTGGTGGTACAAGGCAGAGGGAAATTTGAGGAGCTAATGGTGTGTT 2776
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Db   2701 TGGATGCAGCTGATCTGGTGGTACAAGGCAGAGGGAAATTTGAGGAGCTAATGGTGTGTT 2760

Qy   2777 CTCATGAAATTGCTGCTAGCACAGCCCAGCTTGTGGCTGCATCCAAGGTGAAAGCTGATA 2836
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Db   2761 CTCATGAAATTGCTGCTAGCACAGCCCAGCTTGTGGCTGCATCCAAGGTGAAAGCTGATA 2820

Qy   2837 AGGACAGCCCCAACCTAGCCCAGCTGCAGCAGGCCTCTCGGGGAGTGAACCAGGCCACTG 2896
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Qy    2897  CCGGCGTTGTGGCCTCAACCATTTCCGGCAAATCACAGATCGAAGAGACAGACAACATGG 2956
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Qy    2957  ACTTCTCAAGCATGACGCTGACACAGATCAAACGCCAAGAGATGGATTCTCAGGTTAGGG 3016
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2941  ACTTCTCAAGCATGACGCTGACACAGATCAAACGCCAAGAGATGGATTCTCAGGTTAGGG 3000

Qy    3017  TGCTAGAGCTAGAAAATGAATTGCAGAAGGAGCGTCAAAAACTGGGAGAGCTTCGGAAAA 3076
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Db    3001  TGCTAGAGCTAGAAAATGAATTGCAGAAGGAGCGTCAAAAACTGGGAGAGCTTCGGAAAA 3060

Qy    3077  AGCACTACGAGCTTGCTGGTGTTGCTGAGGGCTGGGAAGAAGGAACAGAGGCATCTCCAC 3136
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Db    3061  AGCACTACGAGCTTGCTGGTGTTGCTGAGGGCTGGGAAGAAGGAACAGAGGCATCTCCAC 3120

Qy    3137  CTACACTGCAAGAAGTGGTAACCGAAAAAGAATAGAGCCAAACCAACACCCCATATGTCA 3196
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Db    3121  CTACACTGCAAGAAGTGGTAACCGAAAAAGAATAGAGCCAAACCAACACCCCATATGTCA 3180

Qy    3197  GTGTAAATCCTTGTTACCTATCTCGTGTGTGTTATTTCCCCAGCCACAGGCCAAATCCTT 3256
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3181  GTGTAAATCCTTGTTACCTATCTCGTGTGTGTTATTTCCCCAGCCACAGGCCAAATCCTT 3240

Qy    3257  GGAGTCCCAGGGGCAGCCACACCACTGCCATTACCCAGTGCCGAGGACATGCATGACACT 3316
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Db    3241  GGAGTCCCAGGGGCAGCCACACCACTGCCATTACCCAGTGCCGAGGACATGCATGACACT 3300

Qy    3317  TCCAAAGACTCCCTCCATAGCGACACCCTTTCTGTTTGGACCCATGG 3363
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Db    3301  TCCAAAGACTCCCTCCATAGCGACACCCTTTCTGTTTGGACCCATGG 3347
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RESULT 2
US-10-750-185-64852
; Sequence 64852, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 64852
;   LENGTH: 3391
;   TYPE: DNA
;   ORGANISM: Bovine 19866880385058

US-10-750-185-64852

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  Query Match               0.7%;  Score 30;  DB 6;  Length 3391;
  Best Local Similarity   100.0%;  Pred. No. 0.00021;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;


Qy       660 AGTATTCAACTCCCTGGACATGTCCCGCTC 689
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Db       669 AGTATTCAACTCCCTGGACATGTCCCGCTC 698
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RESULT 3
US-10-750-623-64852
; Sequence 64852, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 64852
;   LENGTH: 3391
;   TYPE: DNA
;   ORGANISM: Bovine 19866880385058
US-10-750-623-64852

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  Query Match               0.7%;  Score 30;  DB 6;  Length 3391;
  Best Local Similarity   100.0%;  Pred. No. 0.00021;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;


Qy       660 AGTATTCAACTCCCTGGACATGTCCCGCTC 689
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Db       669 AGTATTCAACTCCCTGGACATGTCCCGCTC 698
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RESULT 4
US-10-775-169-259
; Sequence 259, Application US/10775169
; Publication No. US20050287532A9
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael
; APPLICANT: Twine, Natalie
; APPLICANT: Dorner, Andrew
; APPLICANT: Trepicchio, William
; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo

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;   FILE REFERENCE: AM101080 (031896-013000)   .
;   CURRENT APPLICATION NUMBER: US/10/775,169
;   CURRENT FILING DATE:  2004-02-11
;   NUMBER OF SEQ ID NOS: 5278
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 259
;    LENGTH: 4457
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-10-775-169-259

   Query Match              0.6%;  Score 29;  DB 6;  Length 4457;
   Best Local Similarity   100.0%;  Pred. No. 0.00063;
   Matches   29;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;


Qy      2680 GCCTCCAAGGCTGTGGGCTGGGGAGCCAC 2708
             |||||||||||||||||||||||||||||
Db      2670 GCCTCCAAGGCTGTGGGCTGGGGAGCCAC 2698



RESULT 5
US-11-121-849-111397
; Sequence 111397, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
;   APPLICANT: John Palma
;   TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin
Embedded Samples on
;   TITLE OF INVENTION:  Microarrays
;   FILE REFERENCE: 3684.1
;   CURRENT APPLICATION NUMBER: US/11/121,849
;   CURRENT FILING DATE:  2005-05-03
;   PRIOR APPLICATION NUMBER: 60/567,949
;   PRIOR FILING DATE: 2004-05-03
;   NUMBER OF SEQ ID NOS: 673904
;   SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 111397
;    LENGTH: 25
;    TYPE: DNA
;    ORGANISM: Homo sapien
US-11-121-849-111397

   Query Match              0.6%;  Score 25;  DB 7;  Length 25;
   Best Local Similarity  ·100.0%;  Pred. No. 0.069;
   Matches   25;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;


Qy      4184 GACTGTTACTGACTTGGATCCCAAA 4208
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Db         1 GACTGTTACTGACTTGGATCCCAAA 25



RESULT 6
US-11-121-849-111398
; Sequence 111398, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
;   APPLICANT: John Palma
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  Query Match   0.6%; Score 25; DB 7; Length 25;
  Best Local Similarity   100.0%; Pred. No. 0.069;
  Matches   25; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   4221 TTTGGAGCTCTTGGGTCAGAGAAAA 4245
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Db   1 TTTGGAGCTCTTGGGTCAGAGAAAA 25

RESULT 7
US-11-121-849-111399
; Sequence 111399, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin
Embedded Samples on
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 111399
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-11-121-849-111399

  Query Match   0.6%; Score 25; DB 7; Length 25;
  Best Local Similarity   100.0%; Pred. No. 0.069;
  Matches   25; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   4297 GCTCTCGCTGCCCTGTGGACAGGAT 4321
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Db   1 GCTCTCGCTGCCCTGTGGACAGGAT 25

RESULT 8

US-11-121-849-111400
; Sequence 111400, Application US/11121849   -
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin
Embedded Samples on
; TITLE OF INVENTION: Microarrays
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 111400
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-11-121-849-111400

   Query Match   0.6%; Score 25; DB 7; Length 25;
   Best Local Similarity   100.0%; Pred. No. 0.069;
   Matches   25; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   4323 AGGACAGAGGGCACATGAACAGCTT 4347
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Db   1 AGGACAGAGGGCACATGAACAGCTT 25

                        GenCore version 5.1.6
                 Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Searched: 41078325 seqs, 23393541228 residues

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        and is derived by analysis of the total score distribution.

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       32    434    9.6    2561  11   DQ050140               DQ050140 Pan trogl
       33    430    9.5     607   5   BX951152               BX951152 DKFZp781E
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ALIGNMENTS

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DEFINITION Homo sapiens HIP1 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   DQ050139
VERSION   DQ050139.1 GI:66903338
KEYWORDS   GSS.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 2730)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE   A Scan for Positively Selected Genes in the Genomes of Humans and
            Chimpanzees
  JOURNAL   (er) PLoS Biol. 3 (6), E170 (2005)
   PUBMED   15869325
REFERENCE   2 (bases 1 to 2730)
  AUTHORS   Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE   Direct Submission
  JOURNAL   Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT   This sequence was made by sequencing genomic exons and ordering
            them based on alignment. Translation starts at the beginning of
            alignment.
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                     /locus_tag="HC18136"
ORIGIN

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Best Local Similarity   100.0%;  Pred. No. 0;
Matches 1739;  Conservative     0;  Mismatches     0;  Indels     0;  Gaps     0;

Qy      1433 GGAAAGCTCAAGCCAATGAACAGCGATATAGCAAGCTAAAGGAGAAGTACAGCGAGCTGG 1492
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Db       992 GGAAAGCTCAAGCCAATGAACAGCGATATAGCAAGCTAAAGGAGAAGTACAGCGAGCTGG 1051

Qy      1493 TTCAGAACCACGCTGACCTGCTGCGGAAGAATGCAGAGGTGACCAAACAGGTGTCCATGG 1552
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1052 TTCAGAACCACGCTGACCTGCTGCGGAAGAATGCAGAGGTGACCAAACAGGTGTCCATGG 1111

Qy      1553 CCAGACAAGCCCAGGTAGATTTGGAACGAGAGAAAAAAGAGCTGGAGGATTCGTTGGAGC 1612
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Db      1112 CCAGACAAGCCCAGGTAGATTTGGAACGAGAGAAAAAAGAGCTGGAGGATTCGTTGGAGC 1171

Qy      1613 GCATCAGTGACCAGGGCCAGCGGAAGACTCAAGAACAGCTGGAAGTTCTAGAGAGCTTGA 1672
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Db      1172 GCATCAGTGACCAGGGCCAGCGGAAGACTCAAGAACAGCTGGAAGTTCTAGAGAGCTTGA 1231

Qy      1673 AGCAGGAACTTGCCACAAGCCAACGGGAGCTTCAGGTTCTGCAAGGCAGCCTGGAAACTT 1732
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1232 AGCAGGAACTTGCCACAAGCCAACGGGAGCTTCAGGTTCTGCAAGGCAGCCTGGAAACTT 1291

Qy      1733 CTGCCCAGTCAGAAGCAAACTGGGCAGCCGAGTTCGCCGAGCTAGAGAAGGAGCGGGACA 1792
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Db      1292 CTGCCCAGTCAGAAGCAAACTGGGCAGCCGAGTTCGCCGAGCTAGAGAAGGAGCGGGACA 1351

Qy      1793 GCCTGGTGAGTGGCGCAGCTCATAGGGAGGAGGAATTATCTGCTCTTCGGAAAGAACTGC 1852
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Qy      1853 AGGACACTCAGCTCAAACTGGCCAGCACAGAGGAATCTATGTGCCAGCTTGCCAAAGACC 1912
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Db      1412 AGGACACTCAGCTCAAACTGGCCAGCACAGAGGAATCTATGTGCCAGCTTGCCAAAGACC 1471

Qy      1913 AACGAAAAATGCTTCTGGTGGGGTCCAGGAAGGCTGCGGAGCAGGTGATACAAGACGCCC 1972
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RESULT 2
CD251809
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DEFINITION  AGENCOURT_14205955 NIH_MGC_180 Homo sapiens cDNA clone
            IMAGE:30383286 5', mRNA sequence.
ACCESSION   CD251809
VERSION     CD251809.1  GI:31012275
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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            Hominidae; Homo.
REFERENCE   1  (bases 1 to 867)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Michael Brownstein
             cDNA Library Preparation: Invitrogen Corp
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM446  row: o  column: 07
            High quality sequence start: 3
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FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /clone="IMAGE:30383286"
                     /lab_host="DH10B-Ton A ( T1 and T5 phage resistances)"
                     /clone_lib="NIH_MGC_180"
                     /note="Organ: Testis; Vector: pCMV-SPORT6.1; Site_1: NotI;
                     Site_2: EcoRV (destroyed); Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed upon
                     cloning). Average insert size 1.68 kb. Library was
                     constructed by (Invitrogen). Note: this is a NIH_MGC
                     Library."
ORIGIN

  Query Match                17.8%;  Score 809;  DB 6;  Length 867;
  Best Local Similarity      100.0%;  Pred. No. 0;
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Matches 809; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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